

FIGURE 1

801 MetLysHisLeuTrp
ATGAAGCATCTGTG
TACTTCGTAGACAC

851 • PhePheLeuLeuLeuValAlaAlaProArgTrpValLeuSerGlnValGln
GTTCTTCCTTCTCCTAGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGC
CAAGAAGGAAGAGGATCACCGTCGAGGGTCTACCCAGGACAGGGTCCACG

901 • • LeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSer
AGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGAGACCCTGTCC
TCGACGTCCTCAGCCCGGGTCTGACCACTTCGGAAGCCTCTGGGACAGG

951 LeuThrCysThrValSerGlyAlaSerIleSerSerTyrTyrTrpSerTrp
CTCACCTGCACGTGTCTCTGGTGCCTCCATCAGTAGTTACTACTGGAGCTG
GAGTGGACGTGACAGAGACCACGGAGGTAGTCATCAATGATGACCTCGAC

1001 • IleArgGlnProProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrTyr
GATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATT
CTAGGCCGTGCGGGGTCCCTTCCCTGACCTCACCTAACCCATATAGATAA

1051 • • SerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle
ACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATA
TGTCACCCTCGTGGTTGATGTTGGGGAGGGAGTTCTCAGCTCAGTGGTAT

1101 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuArgSerValThr
TCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGAC
AGTCATCTGTGCAGGTTCTTGGTCAAGAGGGACTTCGACTCCAGACACTG

1151 • AlaAlaAspThrAlaValTyrTyrCysAlaArgGluArgLeuGlyIleGly
CGCTGCGGACACGCGCGTGATTACTGTGCGAGAGAGCGACTGGGGATCG
GCGACGCCTGTGCCGGCACATAATGACACGCTCTCTCGCTGACCCCTAGC

1201 • • AspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThr
GGGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC
CCCTGATGACCCCGGTTCTTGGGACCAGTGGCAGAGGAGTCGGAGGTGG

1251 LysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu
AAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCTAGAAAGCACCTCCGA
TTCCCGGGTAGCCAGAAGGGGGACCGCGGGACGAGATCTTCGTGGAGGCT

1301 • SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProVal
GAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG
CTCGTGTGCGCGGGACCCGACGGACCAGTTCCTGATGAAGGGGCTTGCC

1351 ••ThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhe
 TGACGGTGTCGTGGAACCTCAGGCGCTCTGACCAGCGCGTGCACACCTTC
 ACTGCCACAGCACCTTGAGTCCGCGAGACTGGTCGCCGCACGTGTGGAAG

1401 ProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThr
 CCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC
 GGTGACAGGATGTCAGGAGTCCTGAGATGAGGGAGTCGTCGCACCACTG

1451 •ValProSerSerAsnPheGlyThrGlnThrTyrThrCysAsnValAspHis
 CGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATC
 GCACGGGAGGTGTTGAAGCCGTGGGTCTGGATGTGGACGTTGCATCTAG

1501 ••LysProSerAsnThrLysValAspLysThrVal
 ACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCT
 TGTTCGGGTCGTTGTGGTTCCACCTGTTCTGTCAACCACTCTCCGGTCGA

1551 CAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGA
 GTCCCTCCCTCCACAGACGACCTTCGGTCCGAGTCGGGAGGACGGACCT

1601 CGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCATC
 GCGTGGGGCCGACACGTCGGGGTCGGGTCCCGTCGTTCCGTCCGGGGTAG

1651 TGTCTCTCACCCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAG
 ACAGAGGAGTGGGCCTCCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTC

1701 GGTCTTCTGGCTTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCC
 CCAGAAGACCGAAAAAGGTGGTCCGAGGTCCGTCCGTGTCCGACCCACGG

1751 CCTACCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGC
 GGATGGGGTCCGGGAAGTGTGTGTCCCCGTCCACGAACCGAGTCTGGACG

1801 CAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAA
 GTTTTCGGTATAGGCCCTCCTGGGACGGGGACTGGATTGCGCTGGGGTTT

1851 GGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCAGATC
 CCGGTTTGACAGGTGAGGGAGTCGAGCCTGTGGAAGAGAGGAGGGTCTAG

1901 GluArgLysCysCysValGluCys
 CGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTGAGTG
 GCTCATTGAGGGTTAGAAGAGAGACGTCTCGCGTTTACAACACAGCTCAC

1951 •ProProCysPro
 CCCACCGTGCCAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGC
 GGGTGGCACGGGTCCATTGCGTCGGGTCCGGAGCGGGAGGTGAGTTCCG

2001 GGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGG
 CCCTGTCCACGGGATCTCATCGGACGTAGGTCCCTGTCCGGGGTTCGACCC

AlaProProValAlaGlyPro

2051 TGCTGACACGTCCACCTCCATCTCTTCCTCAGCACACCTGTGGCAGGAC
ACGACTGTGCAGGTGGAGGTAGAGAAGGAGTCGTGGTGGACACCGTCCTG

••SerValPheLeuPheProProLysProLysAspThrLeuMetIleSer

2101 CGTCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCTCATGATCTCC
GCAGTCAGAAGGAGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGG

ArgThrProGluValThrCysValValValAspValSerHisGluAspPro

2151 CGGACCCCTGAGGTACAGTGCCTGGTGGTGGACGTGAGCCACGAAGACCC
GCCTGGGGACTCCAGTGCACGCACCACCACCTGCACTCGGTGCTTCTGGG

•GluValGlnPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLys

2201 CGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA
GCTCCAGGTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT

••ThrLysProArgGluGluGlnPheAsnSerThrPheArgValValSer

2251 AGACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGC
TCTGTTTCGGTGCCCTCCTCGTCAAGTTGTCGTCAAGGCACACCAAGTCG

ValLeuThrValValHisGlnAspTrpLeuAsnGlyLysGluTyrLysCys

2301 GTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTG
CAGGAGTGGCAACACGTGGTCTTGACCGACTTGCCGTTCTCATGTTTAC

•LysValSerAsnLysGlyLeuProAlaProIleGluLysThrIleSerLys

2351 CAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCA
GTTCCAGAGGTTGTTTCCGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT

••ThrLys

2401 AAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCG
TTTGGTTTCCACCCTGGGCGCCCCATACTCCCGGTGTACCTGTCTCCGGC

2451 GCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCC
CGAGCCGGGTGGGAGACGGGACCCCTCACTGGCGACACGGTTGGAGACAGG

GlyGlnProArgGluProGlnValTyrThrLeuProProSerArg

2501 CTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GATGTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCC

GluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPhe

2551 GAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTT
CTCCTCTACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAAGTTCCGAA

•TyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsn

2601 CTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA
GATGGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCT

2651 ••AsnTyrLysThrThrProProMetLeuAspSerAspGlySerPhePhe
ACAAC TACAAGACCAACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC
TGTTGATGTTCTGGTGTGGAGGGTACGACCTGAGGCTGCCGAGGAAGAAG

2701 LeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnVal
CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGT
GAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCA

2751 •PheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLys
CTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA
GAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT

2801 ••SerLeuSerLeuSerProGlyLys
AGAGCCTCTCCCTGTCTCCGGGTAAA
TCTCGGAGAGGGACAGAGGCCCATTT

FIGURE 2

901 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrp
 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCT
 TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACGACGAGA

951 ··PheProGlyAlaArgCysLysLeuAspIleGlnLeuThrGlnSerPro
 GGTTCCCAGGTGCCAGGTGTAAGCTTGACATCCAGCTGACCCAATCTCCA
 CCAAGGTCCACGGTCCACATTGGAAGTGTAGGTCGACTGGGTAGAGGT

1001 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
 TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
 AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCCG

1051 ·SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
 AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
 TTCAGTCCCATAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

1101 ··AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
 AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
 TTCGGGGATTTCGGGACTAGATACGACGTAGGTCAAACGTTTCACCCAG

1151 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
 CCATCAAGGTTACGCGGAGTGGATCTGGGACAGAATTCCTCTCACAAT
 GGTAAGTTCCAAGTCGCCGTACCTAGACCCTGTCTTAAGTGAGAGTGTTA

1201 ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
 CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
 GTCGTCGGACGTGCGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

1251 ··ThrTyrProProThrPheGlyGlnGlyThrLysValGluIleLysArg
 ATACTTACCCTCCGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAAACGA
 TATGAATGGGAGGCTGCAAGCCGTTCCCTGGTTCCACCTTTAGTTTGCT

1301 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
 ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
 TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

1351 ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
 GAAATCTGGAAGTCTAGCGTTGTGTGCTGCTGAATAACTTCTATCCCA
 CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

1401 ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
 GAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAAC
 CTCTCCGTTTTCATGTACCTTCCACCTATTGCGGGAGGTAGCCCATTG

1451 SerGlnGluSer
TCCCAGGAGAGT
AGGGTCCTCTCA

FIGURE 3

801	MetGluLeuGlyLeu ATGGAATTGGGGCT TACCTTAACCCCGA
851	•ArgTrpValPheLeuValAlaLeuLeuArgGlyValGlnCysGlnValGln CCGCTGGGTTTTCTCTGTTGCTCTTTTAAGAGGTGTCCAGTGTCCAGGTGC GGCGACCCAAAAGGAGCAACGAGAAAATTCTCCACAGGTCACAGTCCACG
901	••LeuValGluSerGlyGlyGlyValValGlnProGlyArgSerLeuArg AGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGA TCGACCACCTCAGACCCCCTCCGCACCAGGTCGGACCCTCCAGGGACTCT
951	LeuSerCysValAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrp CTCTCCTGTGTAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCACTG GAGAGGACACATCGGAGACCTAAGTGAAGTCATCGATAACCGTACGTGAC
1001	•ValArgGlnAlaProGlyLysGlyLeuGluTrpValAlaValIleSerTyr GGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCAT CCAGGCGGTCCGAGGTCCGTTCCCCGACCTCACCCACCGTCAATATAGTA
1051	••AspGlySerAsnLysTyrTyrAlaAspSerValLysGlyArgPheThr ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCC TACTACCTTCATTATTTATGATACGTCTGAGGCACTTCCCGGCTAAGTGG
1101	IleSerArgAspAsnSerLysAsnThrLeuTyrLeuGlnMetAsnSerLeu ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCT TAGAGGTCTCTGTTAAGGTTCTTGTGCGACATAGACGTTTACTTGTGCGA
1151	•ArgValGluAspThrAlaValTyrTyrCysAlaArgAspHisGlyGlyArg GAGAGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGA CTCTCAACTCCTGTGCCGACACATAATGACACGCTCTCTAGTGCCACCCT
1201	••TyrValTyrAspTyrGlyMetAspValTrpGlyGlnGlyThrThrVal GGTACGTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTC CCATGCAGATGCTGATGCCATACCTGCAGACCCCGGTTCCCTGGTGCCAG
1251	ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaPro ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCC TGGCAGAGGAGTCGGAGGTGGTTCCCGGCTAGCCAGAAGGGGGACCGCGG
1301	•CysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCysLeuValLys CTGCTCTAGAAAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGGTCA GACGAGATCTTCGTGGAGGCTCTCGTGTGGCGGGACCCGACGGACCACT

1351 ••AspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu
 AGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCTAGGCGCTCTG
 TCCTGATGAAGGGGCTTGCCACTGCCACAGCACCTTGAGTCCGCGAGAC

1401 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyr
 ACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTA
 TGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAGTCCTGAGAT

1451 •SerLeuSerSerValValThrValProSerSerAsnPheGlyThrGlnThr
 CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGA
 GAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGTTGAAGCCGTGGGTCT

1501 ••TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLys
 CCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAG
 GGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTGTGGTTCCACCTGTTC

1551 ThrVal
 ACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCA
 TGTCACCACTCTCCGGTCGAGTCCCTCCCTCCACAGACGACCTTCGGT

1601 GGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAG
 CCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTGCGGGTCGGGTC

1651 GGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCCG
 CCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGGAGACGGGCG

1701 CCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCA
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1751 GGCAGGCACAGGCTGGGTGCCCCTACCCAGGCCCTTCACACACAGGGGC
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1801 AGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCC
 TCCACGAACCGAGTCTGGACGGTTTTTCGGTATAGGCCCTCCTGGGACGGG

1851 CTGACCTAAGCCGACCCCAAAGGCCAACTGTCCACTCCCTCAGCTCGGA
 GACTGGATTTCGGCTGGGGTTTTCCGGTTTTGACAGGTGAGGGAGTCGAGCCT

1901 CACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGA
 GTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTTAGAAGAGAGACGTCT

1951 •ArgLysCysCysValGluCysProProCysPro
 GCGCAAATGTTGTGTGTCGAGTGCCACCGTGCCAGGTAAGCCAGCCCAGG
 CGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTTCGGTCGGGTCC

Glu

2001 CCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATC
 GGAGCGGGAGGTTCGAGTTCGCCCTGTCCACGGGATCTCATCGGACGTAG

 2051 CAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCT
 GTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGTGGAGGTAGAGAAGGA

 AlaProProValAlaGlyProSerValPheLeuPheProProLysPro
 2101 CAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCAAACCC
 GTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGG

 LysAspThrLeuMetIleSerArgThrProGluValThrCysValValVal
 2151 AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGT
 TTCCTGTGGGAGTACTAGAGGGCTGGGGACTCCAGTGCACGCCACCA

 •AspValSerHisGluAspProGluValGlnPheAsnTrpTyrValAspGly
 2201 GGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACG
 CCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTGC

 ••ValGluValHisAsnAlaLysThrLysProArgGluGluGlnPheAsn
 2251 GCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAAC
 CGCACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTCGTCAAGTTG

 SerThrPheArgValValSerValLeuThrValValHisGlnAspTrpLeu
 2301 AGCACGTTCCGTGTGGTCAGCGTCCTACCGTTGTGCACCAGGACTGGCT
 TCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACACGTGGTCCTGACCGA

 •AsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeuProAlaPro
 2351 GAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCAGCCC
 CTTGCCGTTCTCATGTTACGTTCCAGAGGTTGTTTCCGGAGGGTCGGG

 ••IleGluLysThrIleSerLysThrLys
 2401 CCATCGAGAAAACCATCTCCAAAACCAAGGTGGGACCCGCGGGGTATGA
 GGTAGCTCTTTTGGTAGAGGTTTGGTTTCCACCCTGGGCGCCCCATACT

 2451 GGGCCACATGGACAGAGGCCGGCTCGGCCACCCCTCTGCCCTGGGAGTGA
 CCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGGACCCTCACT

 GlyGlnProArgGluProGlnVal
 2501 CCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACAGGTG
 GGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTTGGTGTCCAC

 TyrThrLeuProProSerArgGluGluMetThrLysAsnGlnValSerLeu
 2551 TACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
 ATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTCTTGGTCCAGTCGGA

•ThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGlu
2601 GACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGG
CTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGCACCTCACCC

••SerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProMetLeu
2651 AGAGCAATGGGCAGCCGAGACAACACTACAAGACCACACCTCCCATGCTG
TCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGTGGAGGGTACGAC

AspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSer
2701 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAG
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTC

•ArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeu
2751 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTC
GTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAG

••HisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys
2801 TGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
ACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT

FIGURE 4

MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPhePro
901 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTCC
TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACGACGAGACCAAGG

••GlySerArgCysAspIleGlnMetThrGlnSerProSerSerValSer
951 CAGGTTCCAGATGCGACATCCAGATGACCCAATCTCCATCTTCCGTGTCT
GTCCAAGGTCTACGCTGTAGGTCTACTGGGTTAGAGGTAGAAGGCACAGA

AlaSerIleGlyAspArgValSerIleThrCysArgAlaSerGlnGlyIle
1001 GCATCTATAGGAGACAGAGTCTCCATCACTTGTCGGGCGAGTCAGGGTAT
CGTAGATATCCTCTGTCTCAGAGGTAGTGAACAGCCCGCTCAGTCCCATA

•SerSerTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProThrLeu
1051 TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTACGC
ATCGTCGACCAATCGGACCATAGTCGTCTTTGGTCCCTTTCGGGGATGCG

••LeuIleTyrAlaAlaSerThrLeuGlnArgGlyValProSerArgPhe
1101 TCCTTATCTATGCTGCATCCACTTTGCAACGTGGGGTCCCATCAAGGTTT
AGGAATAGATACGACGTAGGTGAAACGTTGCACCCAGGGTAGTTCCAAG

SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGln
1151 AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCA
TCGCCGTACCTAGACCCTGTCTAAAGTGAGAGTGGTAGTCGTCGGACGT

•ProGluAspPheAlaThrTyrPheCysGlnGlnAlaAsnSerPheProPhe
1201 GCCTGAAGATTTTGCAACTTACTTTTGCAACAGGCTAACAGTTTCCCAT
CGGACTTCTAAACGTTGAATGAAAACAGTTGTCCGATTGTCAAAGGGTA

••ThrPheGlyProGlyThrLysValAspIleLysArgThrValAlaAla
1251 TCACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGAACTGTGGCTGCA
AGTGAAAGCCGGGACCCTGGTTTCACCTATAGTTTGCTTGACACCGACGT

ProSerValPheIlePheProProSerAspGluGlnLeuLysSerGlyThr
1301 CCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC
GGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTG

•AlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysVal
1351 TGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAG
ACGATCGCAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTC

••GlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSer
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ATGTCACCTTCCACCTATTGCGGGAGGTTAGCCATTGAGGGTCCTCTCA

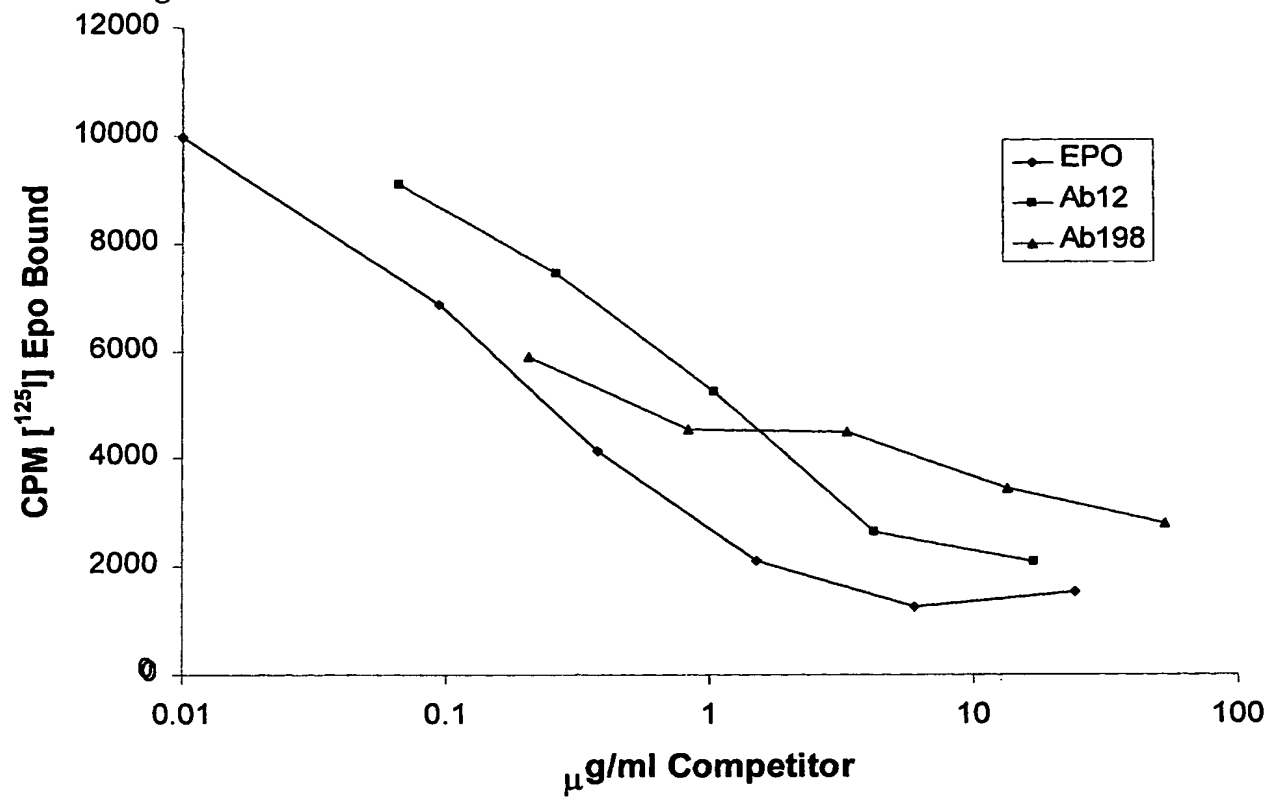
ValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeu
1451 GTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCT
CAGTGTCTCGTCCTGTCGTTCTGTCGTGGATGTCGGAGTCGTCGTGGGA

• ThrLeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGluVal
1501 GACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAG
CTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGATGCGGACGCTTC

• • ThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGly
1551 TCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGA
AGTGGGTAAGTCCCGGACTCGAGCGGGCAGTGTTTCTCGAAGTTGTCCCCT

GluCys
1601 GAGTGT
CTCACA

Figure 5



Erythropoietic Activity of Ab Candidates on F36e Human Erythroleukemic Cell Line

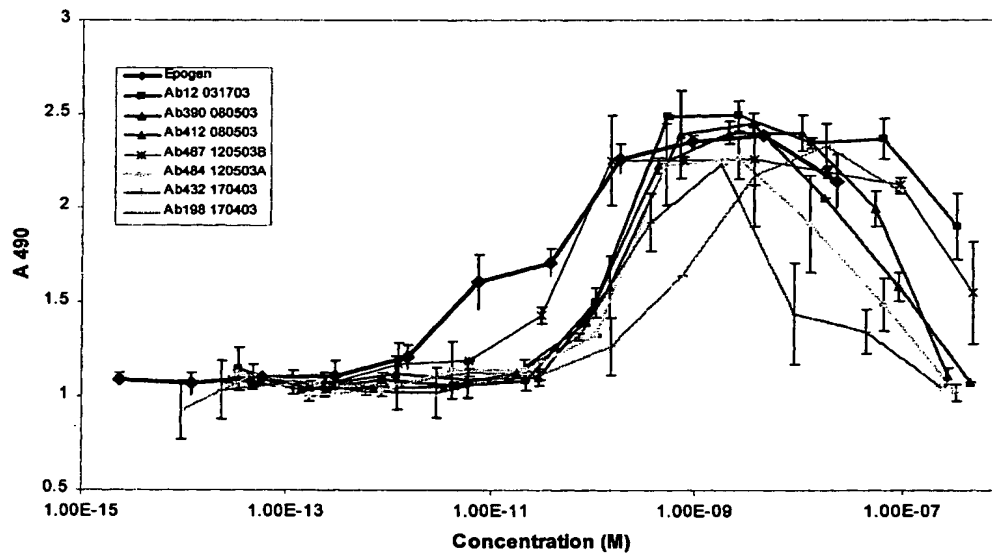


FIGURE 6

Figure 7

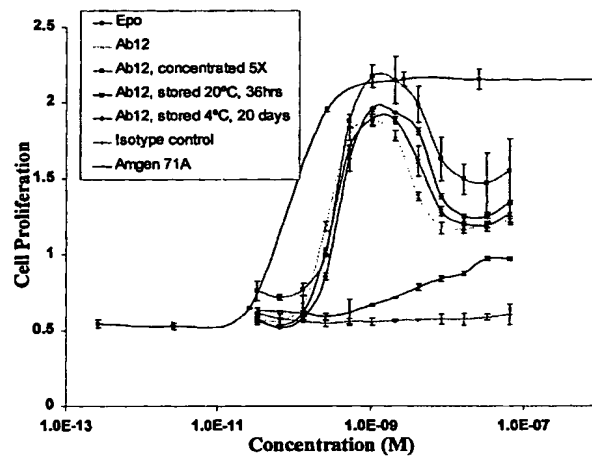
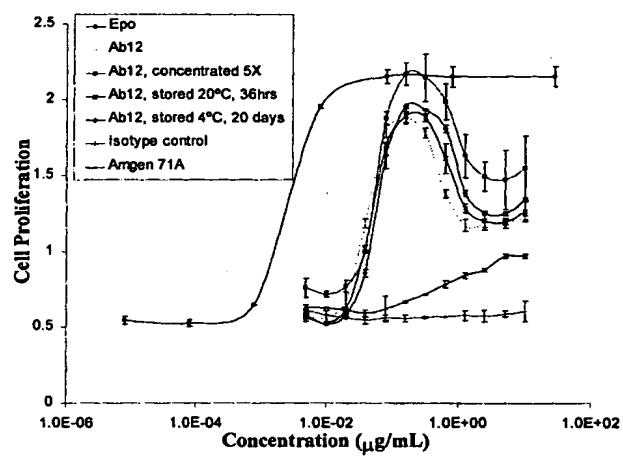


Figure 8

No Epo Control



3 U/ml Epo



150 colonies / dish

500 ng/ml Ab12



48 colonies / dish

Figure 9

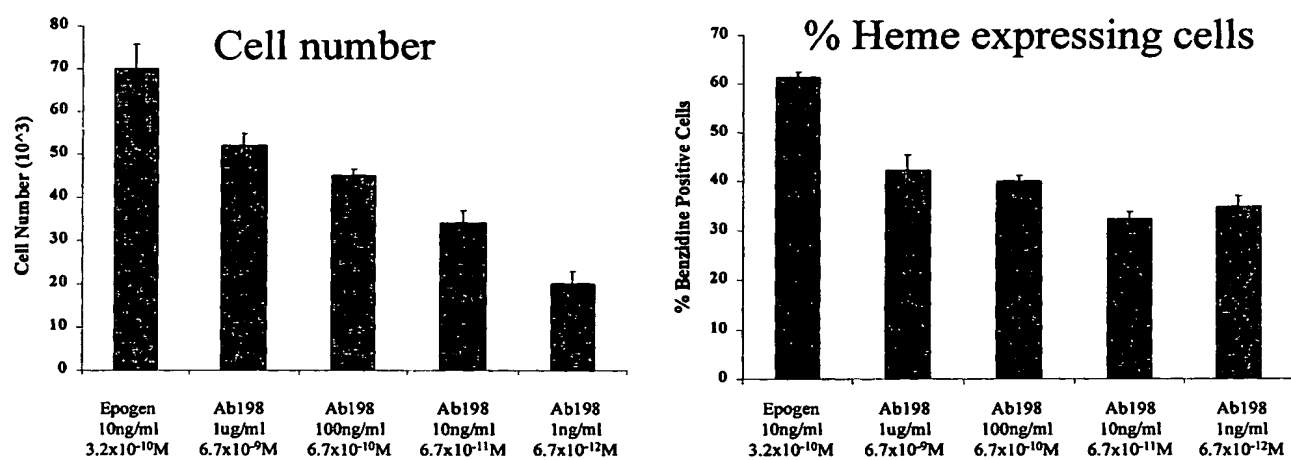
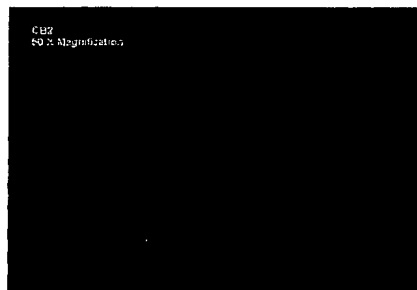
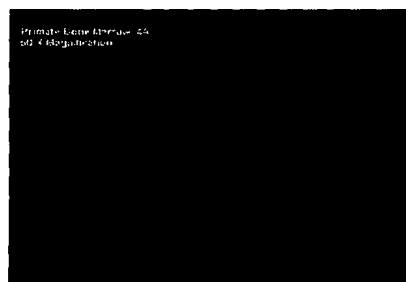


Figure 10

No Epo Control



3 U/ml Epo



3200 ng/ml Ab12



Figure 11

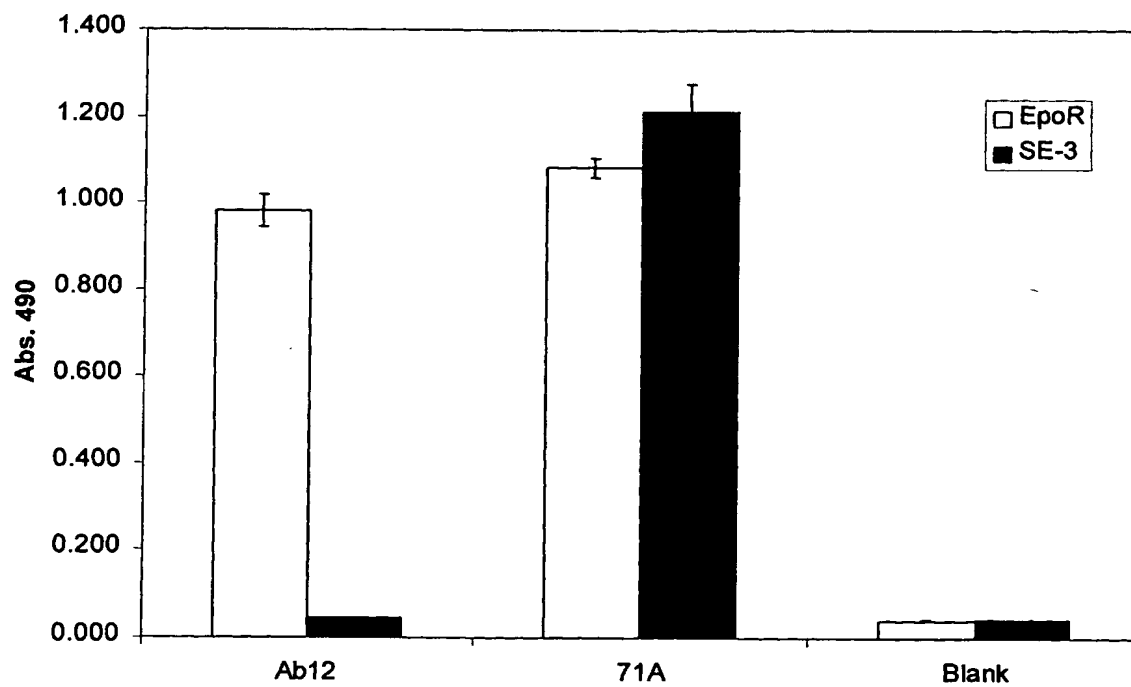


Figure 12

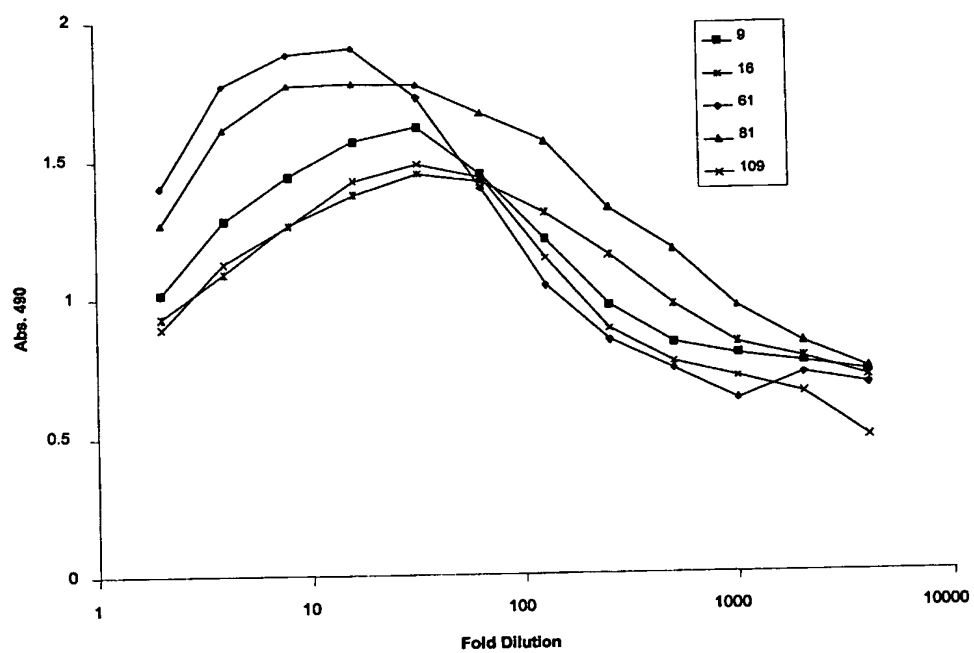


Figure 13

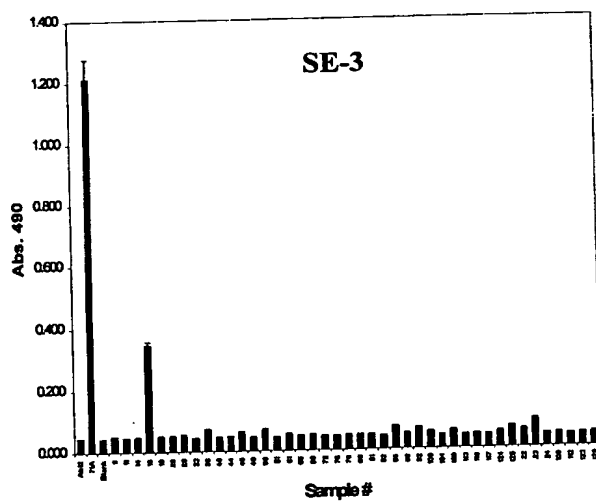
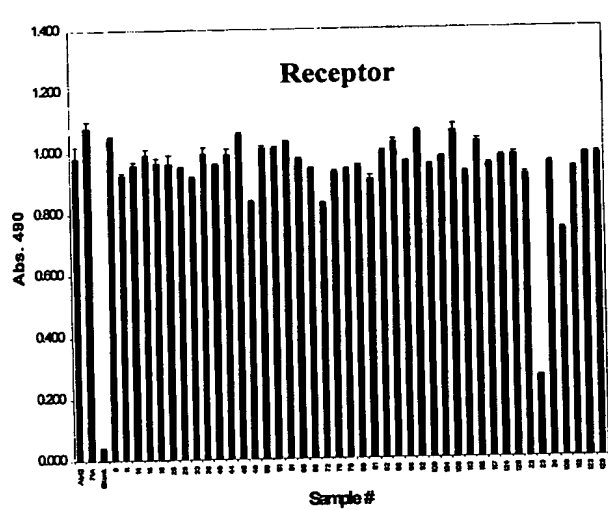


Figure 14

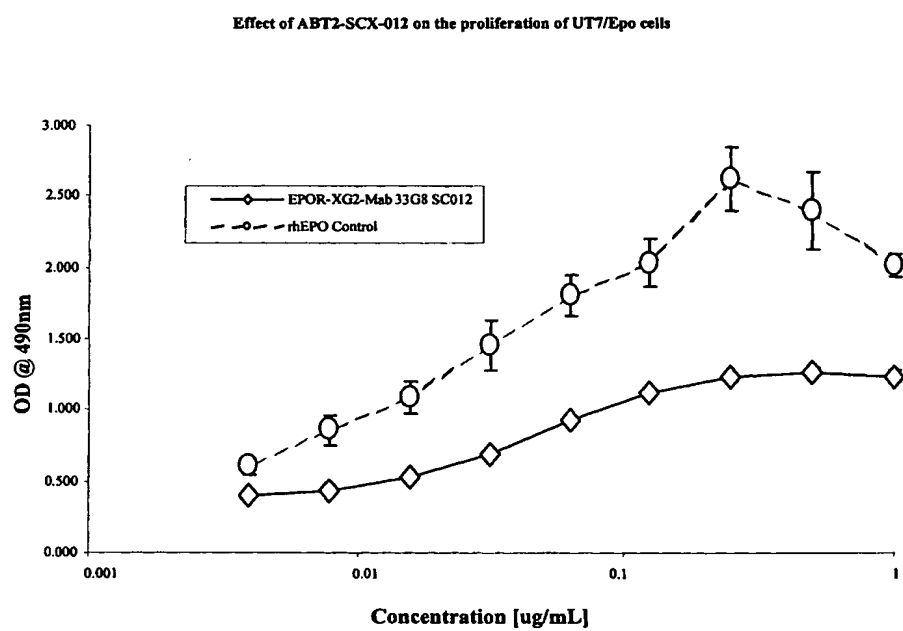


Figure 15

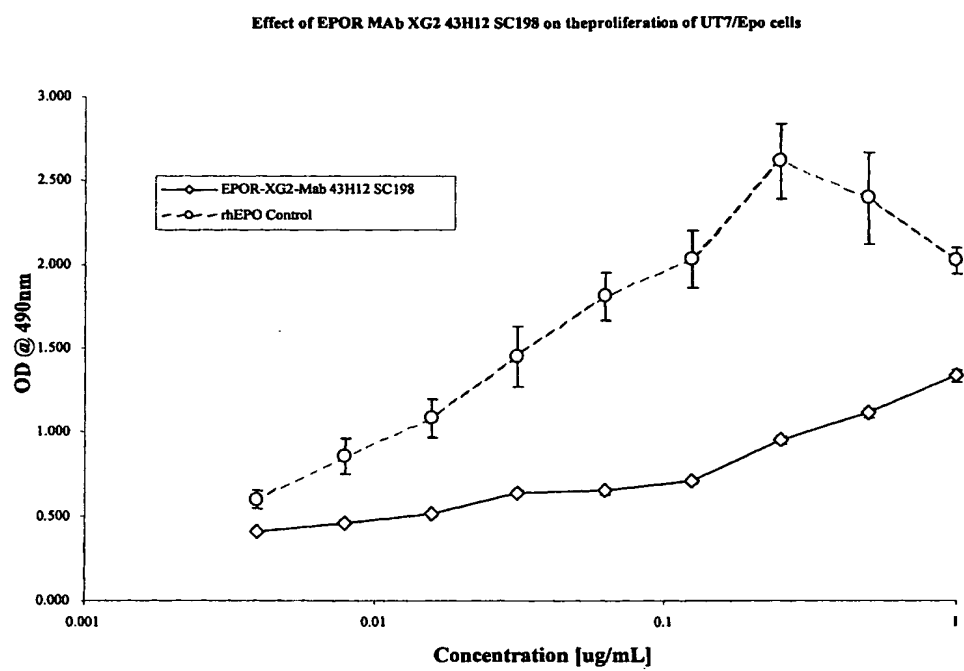


Figure 16

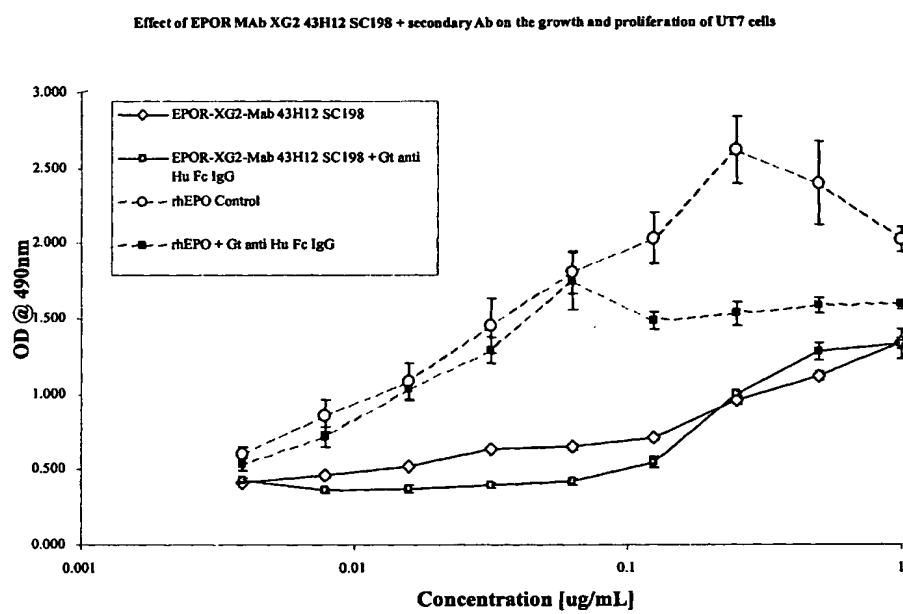


Figure 17

Effect of ABT2-SCX-012 + secondary Ab on the proliferation of UT7/Epo cells

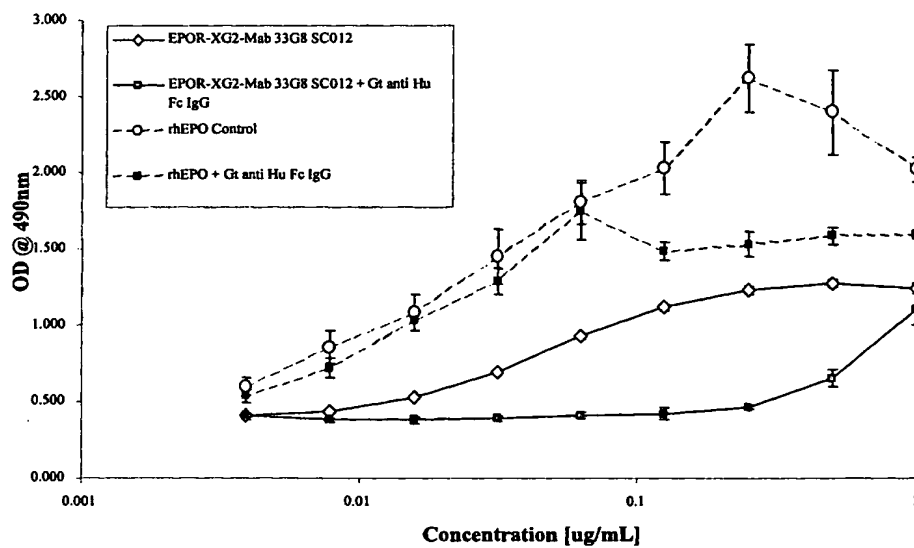


FIGURE 18

A-- ABT2-SCX-003 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG 3'

B-- ABT2-SCX-003 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-003 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCTGGGCGAGTCAGGGTATTAGCAGCTGGTTAGTCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTGCGCTCCTAATCTATGCTGCATCCA
GTTTGCAGCGTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGA
CTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTTT
GTCAACAGGCTAACAGTTTCCCATTCATTTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC3'

D-- ABT2-SCX-003 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGISSWL V WYQQKPGKAPALLIYAASSLQ
RGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 19

A-- ABT2-SCX-012 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACC
CTGTCCCTCACCTGCACTGTCTCTGGTGCCTCCATCAGTAGTTACTACTGGAG
CTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTAT
TACAGTGGGAGCACCAACTACAACCCTCCCTCAAGAGTCGAGTCACCATAT
CAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGACCGC
TGCGGACACGGCCGTGTATTACTGTGCGAGAGAGCGACTGGGGATCGGGGAC
TACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCAG3'

B-- ABT2-SCX-012 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSETLSLTCTVSGASISSYYWSWIRQPPGKGLEWIGYIYYSGS
TNYNPSLKSRTISVDTSKNQFSLKLRSVTAADTAVYYCARERLGIGDYWGQGT
LVTVSS

C-- ABT2-SCX-012 Nucleotide sequence of light chain variable region:

5'GACATCCAGCTGACCCAATCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAG
AATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTAC
TGTCTACAGCATAATACTTACCCTCCGACGTTTCGGCCAAGGGACCAAGGTGG
AAATCAAAC3'

D-- ABT2-SCX-012 Amino acid sequence of light chain variable region:

DIQLTQSPSSLSASVGDRVITTCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQS
GVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNTYPPTFGQGKVEIK

FIGURE 20

A-- ABT2-SCX-022 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGTAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-022 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVVVISY
DGSNKYYADSVKGRFTISRDN SKNTLYQMNSLRVEDTAVYYCARDHGGRVYV
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-022 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-022 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGD RVSITCRASQGISSWLA WYQQKPGKAP TLLIYAASSLQ
RGVPSRFS GSGSGTDFTLTIS SLQPEDFATYFCQQAN SFPFTFGPGTKVDIK

FIGURE 21

A-- ABT2-SCX-054 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTC
CCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAAATATGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTTTATG
GTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACC
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGTCCGTACTACTTTGA
CTACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCAG3'

B-- ABT2-SCX-054 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSKYGMHWVRQAPGKGLEWVAVLW
YDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGPYFDY
WGQGLTVTVSS

C-- ABT2-SCX-054 Nucleotide sequence of light chain variable region:

5'GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAA
GAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGC
CTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCA
TCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGA
CAGACTTCACTGTCAACCATCAGCAGACTGGAACCTGAAGATTTTGCAGTGTAT
TACTGTCAGCAGTATGGTAGTTCACCGTGGACGTTTCGGCCAAGGGACCAAGG
TGGAATCAAAC3'

D-- ABT2-SCX-054 Amino acid sequence of light chain variable region:

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRA
TGIPDRFSGSGSGTDFTVTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

FIGURE 22

A-- ABT2-SCX-060 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-060 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-060 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCCGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCTGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTC AACAGGCTAACAGTTTCCCATTCATTTTCGGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-060 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGISSWLAWYQQKPGKAPTL LIYAASSLQ
RGVPSRFSGSGSGTDFLTISSLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 23

A-- ABT2-SCX-102 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-102 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTTVTVSS

C-- ABT2-SCX-102 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCATTTTCGGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-102 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGISSWLAWYQQKPGKAPKRLIYAASSLQ
RGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 24

A-- ABT2-SCX-135 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG 3'

B-- ABT2-SCX-135 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTITVTVSS

C-- ABT2-SCX-135 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTACATCTGTAGGAGACA
GAGTCTCCATCACTTGTCTGGGCGAGTCAGGGTATTGGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGCAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAACAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCATTTTCGGCCCTGGGACCAAAGTGGA
TGTCAAAC3'

D-- ABT2-SCX-135 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSTSVGDRVSITCRASQGIGSWLAWYQQKPGQAPTLLIYAASSLQ
RGVPSRFSGSGSGTDFLTINS LQPEDFATYFCQQANSFPFTFGPGTKVDVK

FIGURE 25

A-- ABT2-SCX-145 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-145 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTITVTVSS

C-- ABT2-SCX-145 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTGGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGCAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAACAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTC AACAGGCTAACAGTTTCCCATTCATTTTCGGCCCTGGGACCAAAGTGGA
TGTC AAAC3'

D-- ABT2-SCX-145 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGIGSWLAWYQQKPGQAPTLLIYAASSLQ
RGVPSRFSGSGSGTDFTLTINS LQPEDFATYFCQQANSFPFTFGPGTKVDVK

FIGURE 26

A-- ABT2-SCX-198 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGTAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-198 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCVASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-198 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTATAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTACGCTCCTTATCTATGCTGCATCC
ACTTTGCAACGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTC AACAGGCTAACAGTTTCCCATTCAC TTTCCGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-198 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASIGDRVSITCRASQGISSWLAWYQQKPGKAP TLLIYAAS TLQR
GVPSRFSGSGSGTDFLTIS SLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 27

A-- ABT2-SCX-254 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGG
TTTGATGGAAATAATAAATTCTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTCGAGGACACGGCTGTGTATTACTGTGCGCGAGGCGGGAGCTACTGGGAC
TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG3'

B-- ABT2-SCX-254 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWF
DGNKIFYADSVKGRFTISRDN SKNTLYQMNSLRVEDTAVYYCARGGSYWDY
WGQGLTVTVSS

C-- ABT2-SCX-254 Nucleotide sequence of light chain variable region:

5'GATATTGTGATGACCCAGACTCCACTCTTCTCATTTGTCATGATTGGACAGC
CGGCCTCCATCTCCTGCAGGTCTAGGCAAAGCCTCGTACACAGTGATGGAAA
CACCTACTTGAATTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTCCTA
ATTTATAAGACTTCTAACCGGTTCTCTGGGGTCCCAGATAGATTCA GTGGCAG
TGGGGCAGGGACAGATTTCACTGAAAATCAGCAGGGTGGAAGCTGAGGA
TGTCGGGGTTTATTACTGTATGCAAGCTACACAATTCCTATCACGTTCCGCC
AAGGGACACGACTGGAGATTAAA3'

D-- ABT2-SCX-254 Amino acid sequence of light chain variable region:

DIVMTQTPLFSFVMIGQPASISCRS RQSLVHSDGNTYLNWLQQRPGQPPRL LIYKT
SNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFPITFGQGRLEI
K

FIGURE 28

A-- ABT2-SCX-267 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAAAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-267 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCAKDHGGRYV
YDYGMDVWGQGTTVTVSS

C-- ABT2-SCX-267 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTGGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGCAAGCCCCTACGCTCCTAATCTATGCTGCCTCC
AGTTTGCAACGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAACAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTC AACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TGTC AAAC3'

D-- ABT2-SCX-267 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGIGSWLAWYQQKPGQAPTLIIYAASSLQ
RGVPSRFSGSGSGTDFTLTINS LQPEDFATYFCQQANSFPFTFGPGTKVDVK

FIGURE 29

Single Cell	V Heavy/D/J	FR1	CDR1	FR2	CDR2
-	Germline	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA	VISYDGSNKYYADSVKG
3	VH3-30 (V3-30)/D4-23/LH6b	-----V-----	-----	-----	-----
22		-----	-----	-----	-----
60		-----	-----	-----	-----
102		-----	-----	-----	-----
135		-----	-----	-----	-----
145		-----	-----	-----	-----
198		-----V-----	-----	-----	-----
-	Germline	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA	VISYDGSNKYYADSVKG
267	VH3-30.5 (DP-49)/D4-23/JH6b	-----	-----	-----	-----
-	Germline	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA	VISYDGSNKYYADSVKG
54	VH3-33 (DP-50)/DIR3/JH4b	-----	-----K-----	-----	-----L-----
254	VH3-33 (DP-50)/D21-10rc/JH4b	-----	-----	-----	-----F--N--F-----
-	Germline	QVQLQESGGPLVKPSETLSLTCTVS	GGSISSYYWS	WIRQPPGKGLEWIG	YIYSGSTNYPNPSLKS
12	VH4-59 (DP-71)/DIR4rc/JM4a	-----	-----A-----	-----	-----

Single Cell	V Heavy/D/J	FR3	CDR3	FR4
-	Germline	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DHGGRYVYDYGM DV	WGQGTITVTVSS
3	VH3-30 (V3-30)/D4-23/LH6b	-----V-----	-----	-----
22		-----V-----	-----	-----
60		-----V-----	-----	-----
102		-----V-----	-----	-----
135		-----V-----	-----	-----
145		-----V-----	-----	-----
198		-----V-----	-----	-----
-	Germline	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	-----	WGQGTITVTVSS
267	VH3-30.5 (DP-49)/D4-23/JH6b	-----V-----	-----	-----
-	Germline	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	-----	WGQGTITVTVSS
54	VH3-33 (DP-50)/DIR3/JH4b	-----	GPYYFDY	-----
254	VH3-33 (DP-50)/D21-10rc/JH4b	-----V-----	GGSYWDY	-----
-	Germline	RVTISVDTSKNQFSLKLSSTAA DTAVYYCAR	-----	WGQGTITVTVSS
12	VH4-59 (DP-71)/DIR4rc/JM4a	-----R-----	ERLGIGDY	-----

Figure 30

Single Cell	V kappa/J	FR1	CDR1	FR2	CDR2
-	CH1111	KIVLVQSPGTLISLSPGRATLSC	RASQSVSSSYLA	WYQQRFGQAFRLITY	GASSRAT
54	VkIII (A27)/Jk1	-----V-----	-----	-----	-----
-	CH1111	DIQMIVSPSSVSASVGRVTTC	RASQGISWLA	WYQQRFGKAFRLITY	AASSLOS
3	VkI (L5)/Jk3	-----S-----	-----V-----	-----A-----	-----R-----
22		-----S-----	-----	-----T-----	-----R-----
60		-----S-----	-----	-----T-----	-----R-----
102		-----S-----	-----	-----R-----	-----R-----
135		-----T-----S-----	-----G-----	-----Q-----T-----	-----R-----
145		-----S-----	-----G-----	-----Q-----T-----	-----R-----
198		-----I-----S-----	-----	-----T-----	-----T-----R-----
267		-----S-----	-----G-----	-----Q-----T-----	-----R-----
-	CH1111	DIQMIVSPSSVSASVGRVTTC	RASQGISWLA	WYQQRFGKAFRLITY	AASSLOS
12	VkI (A30)/Jk1	---L-----	-----	-----	-----
-	CH1111	DIVMIVTPLSPPTLGPASISC	RSSQSLVHSDGNTYLS	WLOQRFGQPFRLITY	KISKRFIS
254	VkII (A23)/Jk5	-----F-F-MI-----	---R-----M-----	-----	-----T-----

Single Cell	V kappa/J	FR3	CDR3	J
-	CH1111	GIEDRIFSGSGGTDITLTISRLEPEDFAVYYC	QQXGSEFWT	FGQGIVKIK
54	VkIII (A27)/Jk1	-----V-----	-----	-----
-	CH1111	GVPSRIFSGSGGTDITLTISRLEPEDFAVYYC	QQANSEFPTT	FGQIRVDIK
3	VkI (L5)/Jk3	-----F-----	-----	-----
22		-----F-----	-----	-----
60		-----F-----	-----	-----
102		-----F-----	-----	-----
135		-----N-----F-----	-----	-----V-----
145		-----N-----F-----	-----	-----V-----
198		-----F-----	-----	-----
267		-----N-----F-----	-----	-----V-----
-	CH1111	GVPSRIFSGSGGTDITLTISRLEPEDFAVYYC	LQHSYPPTT	FGQIRVDIK
12	VkI (A30)/Jk1	-----	---T-----	-----
-	CH1111	GVEDRIFSGSGGTDITLTISRLEPEDFAVYYC	MQATQFPTT	FGQIRVDIK
254	VkII (A23)/Jk5	-----	-----	-----

Comparison of Erythropoietic Activity of Gamma 1 Ab-12 versus Gamma 2 Ab-12 on F36e Human Erythroleukemic Cell Line

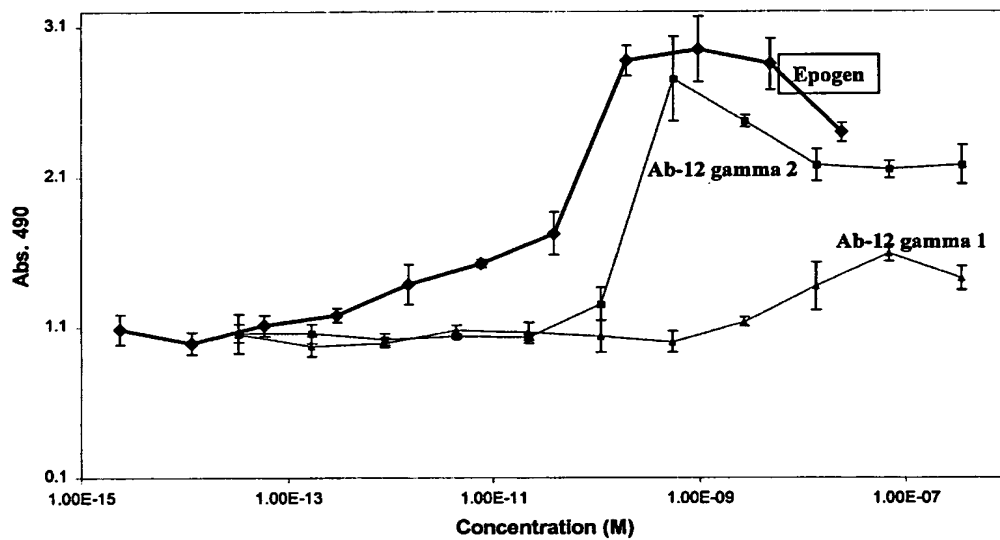
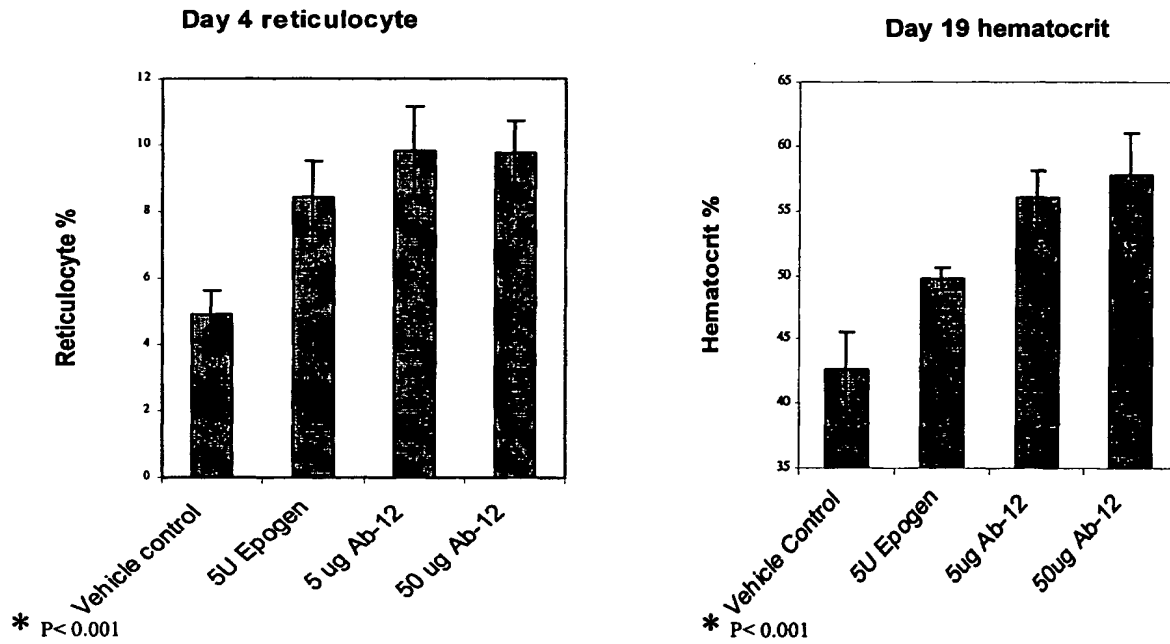


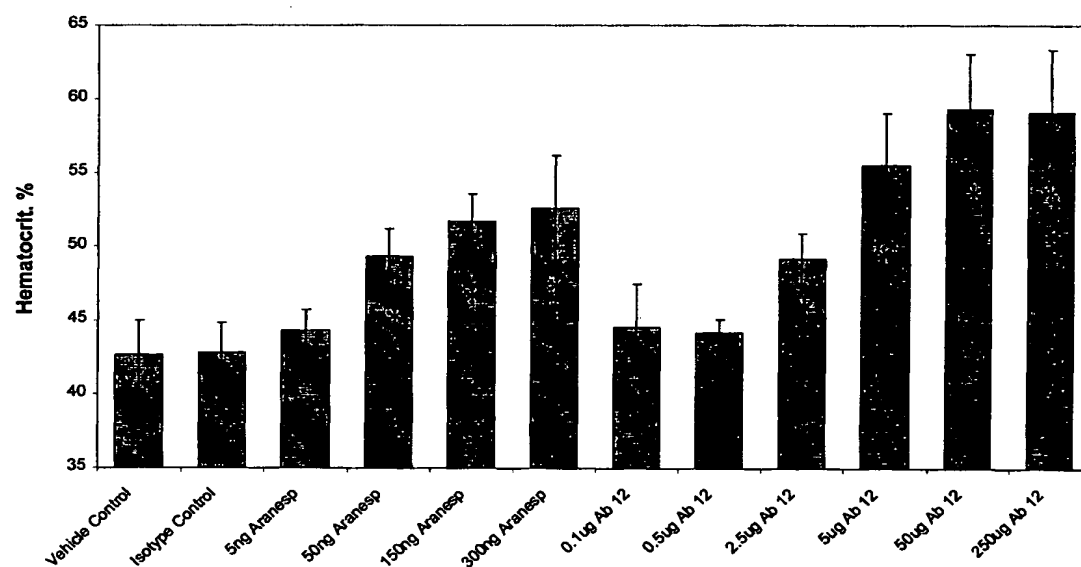
FIGURE 31

FIGURE 32

Ab-12 Increases Reticulocyte Count and Hematocrit in Transgenic Mice



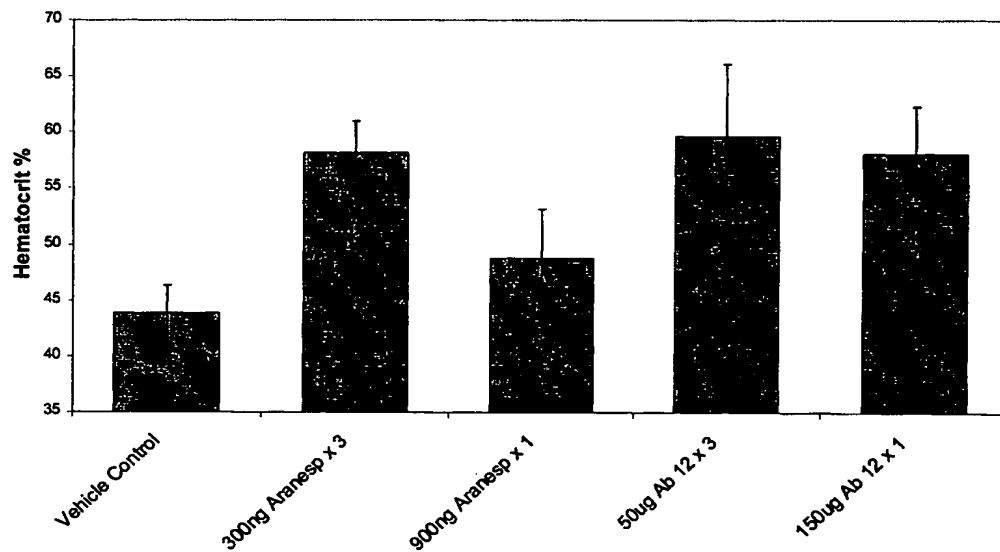
Day 19 Hematocrit in Transgenic Mice Following Weekly Dosing with Ab-12 or Aranesp



* $P < 0.001$

FIGURE 33

Day 19 Hematocrit in Transgenic Mice Comparing Single vs. Weekly Dosing with Ab-12 or Aranesp



* $P < 0.01$

FIGURE 34

FIGURE 35

A. Ab390 nucleotide sequence of heavy chain variable region:

5' CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACC
CTGTCCCTCACCTGCACTGTCTCTGGTGCCTCCATCAGTAATTACTACTGG
AGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATGTC
TCTTACAGTGGGAGTACGTACTACAACCCCTCCCTCAAGGGTCGAGTCACC
ATGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTG
ACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGAGAAAACTGGGGATT
GGAGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA3'

B. Ab390 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSSETLSLTCTVSGASISNYYWSWIRQPPGKGLEWIGYVSYSGS
TYYNPSLKGRVTMSVDTSKNQFSLKLSSVTAADTAVYYCAREKLGIGDYWGQGLV
TVSS

C. Ab390 nucleotide sequence of light chain variable region:

5' GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAAAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAG
AATTCATCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGTTATCCGTGCAGTTTTGGCCAGGGGACCAAGCTG
GAGATCAAAC3'

D. Ab390 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVITICRASQGIKNDLGWYQQKPGKAPKRLIYAASSLQS
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPCSFQGTGLEIK

FIGURE 36

A. Ab412 nucleotide sequence of heavy chain variable region:

5' CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCC
TGTCCTCACCTGCACTGTCTCTGGTGCCTCCATCAGCAGTGGTGCTTACTA
CTGGAGTTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGATTGGGTAC
ATCTATAAGAGTGAGACCTCCTACTACAACCCGTCCCTCAAGAGTCGACTTA
CCCTATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAACCTGATCTCTGT
GACTGCCGCGGACACGGCCGTGTATTATTGTGCGAGAGATAAACTGGGGATC
GCGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA3'

B. Ab412 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSQTLSTCTVSGASISSGAYYWSWIRQHPGKGLEWIGY
IYKSETSYYNPSLKSRLTSLVDTSKNQFSLNLSVTAADTAVYYCARDKLG
ADYWGQGTLLTVSS

C. Ab412 nucleotide sequence of light chain variable region:

5' GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGACATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AATTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAG
AATTCATCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTA
CTGTCTACAGCATAATAGCTACCCTCCCACTTTCGGCGGAGGGACCAAGGTG
GAAATCAAAC3'

D. Ab412 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPGKAPKRLIYAAS
NLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPPTFGGGTKV
EIK

FIGURE 37

A. Ab432 nucleotide sequence of heavy chain variable region:

5' CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCC
TGTCCTCACCTGCACTGTCTCTGGTGTCTCCATCAGTAATTACTACTGGAG
CTGGATCCGGCAGTCCCCAGGGAAGGGACTGGAGTGGATTGGATATATCTAT
TACAGTGGGAGTCCCTATTACAACCCCTCCCTCAAGAGTCGAGTCACTATAT
CTGCAGACACGTCCAAGAACCAATTCTCCCTGAAGCTGAGCTCTGTGACCGC
TGCGGACACGGCCATTTATTACTGTGCGAGAGAAAACTGGGGATTGGAGAC
TACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG3'

B. Ab432 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSSETLSLTCTVSGVSISNYYWSWIRQSPGKGLEWIGYIY
YSGSPYYNP SLKSRVTISADTSKNQFS LKLSSVTAADTAIYYCAREKLGIGD
YWGQGT LVT VSS

C. Ab430 nucleotide sequence of light chain variable region:

5' GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTCTGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAGCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAG
AATTCACCTCTACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGTTACCCTCCCCTTCGGCCCTGGGACCAAGGTG
GATATCAAAC3'

D. Ab430 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS
SLQSGVPSRFS GSGSGTEFTLTIS SLQPEDFATYYCLQHNSYPPTFGPGTKV
DIK

FIGURE 38

A. Ab467 nucleotide sequence of heavy chain variable region:

5' CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCC
TGTCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTCGTTACTACTGGAG
CTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATGTCTCT
TACAGTGGGAGCACCTACTACAACCCCTCCCTCAAGAGTCGAGTCACCATAT
CAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGC
TGCGGACACGGCCGTGTATTACTGTGCGAGAGATAAACTGGGGATTGGAGAC
TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG3'

B. Ab467 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSSETLSLTCTVSGGSISRYYWSWIRQPPGKGLEWIGYVS
YSGSTYYNPSLKSRTISVDTSKNQFSLKLSSVTAADTAVYYCARDKLGIGD
YWGQGTLLVTVSS

C. Ab467 nucleotide sequence of light chain variable region:

5' GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCGGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAG
AATTCATCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGTTACCCGTGCAGTTTTGGCCAGGGGACCAAGCTG
GAGATCAAAC3'

D. Ab467 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS
SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPFSFGQGTKL
EIK

FIGURE 39

A. Ab484 nucleotide sequence of heavy chain variable region:

5' CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTTACAGACCC
TGTCCTTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTGGTGTTTACTA
CTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGATTGGGTAC
ATCTATAACAGTAAGACCTCCTATTATAATCCGTCCCTCAAGAGTCGACTTA
CCCTATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAACCTGATCTCTGT
GACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATAAATTGGGGATC
GCGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG3'

B. Ab484 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPLQTLSTCTVSGGSISSGVYYWSWIRQHPGKGLEWIGY
IYNSKTSYYNPSLKSRLTSLVDTSKNQFSLNLSVTAADTAVYYCARDKLG
ADYWGQGTLLTVSS

C. Ab484 nucleotide sequence of light chain variable region:

5' GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGACAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAG
AATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGCTACCCTCCCACTTTCGGCGGAGGGACCAAGGTG
GAGATCAAAC3'

D. Ab484 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVITICRTSQGIRNDLGWYQQKPGKAPKRLIYAAS
SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPPTFGGGTKV
EIK

Well	Single Cell	Chain ID	V Heavy/D/J	FR1	CDR1	FR2
-	-	-	-	QVQLVESGGGVVQPGSRSLRLSCAAS	GFTFSSTGMH	WVRQAPGKGLNWVA
43H12	198	14325.3	VH3-30/D4-23/JH6	-----V-----	-----V-----	-----V-----
-	-	-	-	QVQLQESGPGLVKPSSETLSLTCTVS	GGSISSYYWS	WIRQPPGKGLEWIG
33G8	12	13308.1	VH4-59/DIR4rc/JH4	-----A-----	-----A-----	-----A-----
-	-	-	-	QVQLQESGPFLLVKPSQTLSLTCTVS	GGSISSGGYYWS	WIRQHPGKGLEWIG
230A4	412	54955.1	V4-31/DIR4rc/JH4	-----G-----	-----A-----	-----A-----
-	-	-	-	QVQLQESGPGLVKPSQTLSLTCTVS	GGSISSGGYYWS	WIRQHPGKGLEWIG
208A12	484	57130.1	V4-30.1/DIR4rc/JH4	-----L-----	-----V-----	-----V-----
-	-	-	-	QVQLQESGPGLVKPSSETLSLTCTVS	GGSISSYYWS	WIRQPPGKGLEWIG
259C12	467	56977.2	V4-59/D7-27/JH4	-----R-----	-----R-----	-----R-----
236D12	390	57141.2	VH4-59/D7-27/JH4b	-----L-----	-A--N----	-----S-----
223H2	432	57354.11	VH4-59/D7-27/JH4b	-----L-----	-V--N----	-----S-----

CDR2	FR3	CDR3	FR4
VISYDGSNKYYADSVKG	RFTISRDNKNTLYLQNNSLRAEDTAVYYCAK	WGQGLTVTVSS	
198	-----V-----R	DHGGRYVYDYGMDV	-----V-----
YIYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSVTAADTAVYYCAR	WGQGLTVTVSS	
16	-----R-----	ERLGTGDY	-----R-----
YIYSGSTIYNPSLKS	RVTISVDTSKNQFSLKLSVTAADTAVYYCAR	WGQGLTVTVSS	
412	-K-DTS-----N-I-----	DKLGIADY	-----V-----
YIYSGSTIYNPSLKS	RVTISVDTSKNQFSLKLSVTAADTAVYYCAR	WGQGLTVTVSS	
484	-N-KTS-----L-L-----	DKLGIADY	-----V-----
YIYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSVTAADTAVYYCAR	WGQGLTVTVSS	
467	-VS-----Y-----	DKLGTGDY	-----R-----
390	-VS-----Y-----G	EKLGTGDY	-----R-----
430	-----PY-----	EKLGTGDY	-----R-----

Figure 40

Well	Single Cell	Chain ID	V Kappa/J	FR1	CDR1	FR2
-	-	14325.3	L5/Jk3	DIQMTQSPSSVSASVGDRTTTC	RASQIISWLA	WTQOKPGKAPKLLIY
43H12	198	14325.3	L5/Jk3	-----I-----S-----	-----T-----	-----
-	-	13308.1	A30/Jk3	DIQMTQSPSSLSASVGDRTTTC	RASQIRNDLG	WTQOKPGKAPKRLIY
3308	12	13308.1	A30/Jk3	-----L-----	-----	-----
223H2	430	54494.1	A30/Jk3	DIQMTQSPSSLSASVGDRTTTC	RASQIRNDLG	WTQOKPGKAPKRLIY
-	-	54732.2	A30 (Vk1) /Jk4	-----D-----	-----	-----
230A4	412	57094.1	A30 (Vk1) /Jk4	DIQMTQSPSSLSASVGDRTTTC	RASQIRNDLG	WTQOKPGKAPKRLIY
-	-	56956.1	A30 (Vk1) /Jk2	-----T-----	-----	-----
208A12	484	56829.3	A30 (Vk1) /Jk2	DIQMTQSPSSLSASVGDRTTTC	RASQIRNDLG	WTQOKPGKAPKRLIY
-	-	-	-	-----K-----	-----	-----
259C12	467	-	-	-	-	-
236D12	390	-	-	-	-	-

CDR2	FR3	CDR3	FR4
AASSLQS	GVPSRFGSGSGTFTLTISLQPEDFATYYC	QGANSPFPT	FGGTRKVDIK
198	-----T---R-----P-----	-----	-----
AASSLQS	GVPSRFGSGSGTFTLTISLQPEDFATYYC	LQHNSYPPT	FGGTRKVBIEK
12	-----	-----T---P-----	-----
430	-----	-----P-----	-----D-----
AASSLQS	GVPSRFGSGSGTFTLTISLQPEDFATYYC	LQHNSYPLT	FGGTRKVBIEK
412	-----N-----	-----P-----	-----
AASSLQS	GVPSRFGSGSGTFTLTISLQPEDFATYYC	LQHNSYPLT	FGGTRKVBIEK
484	-----	-----P-----	-----
AASSLQS	GVPSRFGSGSGTFTLTISLQPEDFATYYC	LQHNSYPLT	FGGTRKVBIEK
464	-----	-----CS-----	-----
390	-----	-----CS-----	-----

Figure 41

FIGURE 42

1 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
ATGAAGCATCTGTGGTTCTTCCTTCTCCTGGTGG
TACTTCGTAGACACCAAGAAGGAAGAGGACCACC

51 ••AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
CAGCTCCCAGATGGGTCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCA
GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCGGT

101 GlyLeuValLysProSerGluThrLeuSerLeuThrCysThrValSerGly
GGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGG
CCTGACCACTTCGGAAGCCTCTGGGACAGGGAGTGGACGTGACAGAGACC

151 •AlaSerIleSerAsnTyrTyrTrpSerTrpIleArgGlnProProGlyLys
TGCCTCCATCAGTAATTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGA
ACGGAGGTAGTCATTAATGATGACCTCGACCTAGGCCGTCGGGGGTCCCT

201 ••GlyLeuGluTrpIleGlyTyrValSerTyrSerGlySerThrTyrTyr
AGGGACTGGAGTGGATTGGGTATGTCTCTTACAGTGGGAGTACGTACTAC
TCCCTGACCTCACCTAACCCTACAGAGAATGTCACCCTCATGCATGATG

251 AsnProSerLeuLysGlyArgValThrMetSerValAspThrSerLysAsn
AACCCTCCCTCAAGGGTCGAGTCACCATGTCTAGTAGACACGTCCAAGAA
TTGGGGAGGGAGTTCACGCTCAGTGGTACAGTCATCTGTGCAGGTTCTT

301 •GlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyr
CCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGT
GGTCAAGAGGGACTTCGACTCGAGACACTGGCGACGCCTGTGCCGGCACA

351 ••TyrCysAlaArgGluLysLeuGlyIleGlyAspTyrTrpGlyGlnGly
ATTACTGTGCGAGAGAAAACTGGGGATTGGAGACTACTGGGGCCAGGGA
TAATGACACGCTCTCTTTTGGACCCCTAACCTCTGATGACCCCGGTCCCT

401 ThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro
ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
TGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCAGAAGGG

451 •LeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCys
CCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCT
GGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTGCGGGGACCCGA

501 ••LeuValLysAspTyrPheProGluProValThrValSerTrpAsnSer
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCA
CGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGT

551 GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer
 GGCCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTC
 CCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAG

601 ·GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGly
 AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCG
 TCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGTTGAAGC

651 ··ThrGlnThrTyrThrCysAsnValAspHisLysProSerAsnThrLys
 GCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAG
 CGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCCGGGTCGTTGTGGTTC

701 ValAspLysThrVal
 GTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGC
 CACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCACAGACG

751 TGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCC
 ACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGG

801 CCAGCCCAGGGCAGCAAGGCAGGCCCATCTGTCTCCTCACCCGGAGGCC
 GGTCCGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGG

851 TCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCAC
 AGACGGGCGGGGTGAGTACGAGTCCCTCTCCAGAAGACCGAAAAAGTG

901 CAGGCTCCAGGCAGGCACAGGCTGGGTGCCCTACCCAGGCCCTTCACA
 GTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGGAAGTGT

951 CACAGGGGCGAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGG
 GTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTCCGGTATAGGCCCTCC

1001 ACCCTGCCCCCTGACCTAAGCCGACCCCAAAGGCCAACTGTCCACTCCCT
 TGGGACGGGGACTGGATTCCGGCTGGGGTTTTCCGGTTTGACAGGTGAGGGA

1051 CAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCT
 GTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTTAGAAGA

1101 GluArgLysCysCysValGluCysProProCysPro
 CTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCACCGTGCCAGGTAAGC
 GAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCCG

1151 CAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTA
 GTCGGGTCCGGAGCGGGAGGTGAGTTCCGCCCTGTCCACGGGATCTCAT

1201 GCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCA
 CGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGTGGAGGT

AlaProProValAlaGlyProSerValPheLeuPhePro
 1251 TCTCTTCCTCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTTCCCC
 AGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGG

ProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCys·
 1301 CCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTG
 GGTTCCTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGCAC

·ValValValAspValSerHisGluAspProGluValGlnPheAsnTrpTyr·
 1351 CGTGGTGGTGGACGTGAGCCACGAAGACCCGAGGTCCAGTTCAACTGGT
 GCACCACCACCTGCACCTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCA

··ValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu
 1401 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAG
 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTC

GlnPheAsnSerThrPheArgValValSerValLeuThrValValHisGln·
 1451 CAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTACCGTTGTGCACCA
 GTCAAGTTGTCGTGCAAGGCACACCAAGTCGCAGGAGTGGAACACGTGGT

·AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeu·
 1501 GGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCC
 CCTGACCGACTTGCCGTTCTCATGTTACGTTCCAGAGGTGTTTCCGG

··ProAlaProIleGluLysThrIleSerLysThrLys
 1551 TCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAGGTGGGACCCGC
 AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTGGTTTCCACCCTGGGCG

1601 GGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCCACCCTCTGCCC
 CCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGG

GlyGlnProArgGlu
 1651 TGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA
 ACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTT

ProGlnValTyrThrLeuProProSerArgGluGluMetThrLysAsnGln·
 1701 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
 GGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGT

·ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal·
 1751 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCG
 CCAGTCGGACTGGACGGACAGTTTCCGAAGATGGGGTCGCTGTAGCGGC

··GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro
 1801 TGGAGTGGGAGAGCAATGGGCAGCCGAGACAACACTACAAGACCACACCT
 ACCTACCCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGTGGA

1851 ProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrVal·
CCCATGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGT
GGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCA

1901 ·AspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHis·
GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACG

1951 ··GluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerPro
ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
TACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGC

2001 GlyLys
GGTAAA
CCATTT

FIGURE 43

1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuLeu
ATGAGGCTCCCCGCTCAGCTCCTGGGGCTCCTGC
TACTCCGAGGGGCGAGTCGAGGACCCCGAGGACG

51 ··LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

101 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCCG

151 ·SerGlnGlyIleLysAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
AAGTCAGGGCATTAAAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
TTCAGTCCCGTAATTTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

201 ··AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
TTCGGGGATTTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCAG

251 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
CCATCAAGGTTACGCGGCAGTGGATCTGGGACAGAATTCCTCTCACAAT
GGTAGTTCCAAGTCGCCGTACCTAGACCCTGTCTTAAGTGAGAGTGTTA

301 ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
GTCGTTCGGACGTTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

351 ··SerTyrProCysSerPheGlyGlnGlyThrLysLeuGluIleLysArg
ATAGTTATCCGTGCAGTTTGGCCAGGGGACCAAGCTGGAGATCAAACGA
TATCAATAGGCACGTCAAAACCGGTCCCTGGTTCGACCTCTAGTTTGCT

401 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

451 ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
GAAATCTGGAAGTCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

501 ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC
CTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

551 SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCCTGTCGTGGATGTCGGA

601 ·SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
CAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

651 ··AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTCCTCG

701 PheAsnArgGlyGluCys
TTCAACAGGGGAGAGTGT
AAGTTGTCCCCTCTCACA

FIGURE 44

1 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
ATGAAACATCTGTGGTTCTTCCTCCTGCTGGTGG
TACTTTGTAGACACCAAGAAGGAGGACGACCACC

51 ··AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
CAGCTCCCAGATGGGTCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCCA
GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCCGGT

101 GlyLeuValLysProSerGlnThrLeuSerLeuThrCysThrValSerGly
GGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCTGG
CCTGACCACTTCGGAAGTGTCTGGGACAGGGAGTGGACGTGACAGAGACC

151 ·AlaSerIleSerSerGlyAlaTyrTyrTrpSerTrpIleArgGlnHisPro
TGCTTCCATCAGCAGTGGTGCTTACTACTGGAGTTGGATCCGCCAGCACC
ACGGAGGTAGTCGTCACCACGAATGATGACCTCAACCTAGGCGGTCTGTGG

201 ··GlyLysGlyLeuGluTrpIleGlyTyrIleTyrLysSerGluThrSer
CAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATAAGAGTGAGACCTCC
GTCCCTTCCCGGACCTCACCTAACCCATGTAGATATTCTCACTCTGGAGG

251 TyrTyrAsnProSerLeuLysSerArgLeuThrLeuSerValAspThrSer
TACTACAACCCGTCCCTCAAGAGTCGACTTACCCTATCAGTAGACACGTC
ATGATGTTGGGCAGGGAGTTCTCAGCTGAATGGGATAGTCATCTGTGCAG

301 ·LysAsnGlnPheSerLeuAsnLeuIleSerValThrAlaAlaAspThrAla
TAAGAACCAGTTCTCCCTGAACCTGATCTCTGTGACTGCCGCGGACACGG
ATTCTTGGTCAAGAGGGACTTGGACTAGAGACACTGACGGCGCCTGTGCC

351 ··ValTyrTyrCysAlaArgAspLysLeuGlyIleAlaAspTyrTrpGly
CCGTGTATTATTGTGCGAGAGATAAACTGGGGATCGCGGACTACTGGGGC
GGCACATAATAACACGCTCTCTATTTGACCCCTAGCGCCTGATGACCCCG

401 GlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyProSerVal
CAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT
GTCCCTTGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCA

451 ·PheProLeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeu
CTTCCCCCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCC
GAAGGGGGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTCGGCGGG

501 ··GlyCysLeuValLysAspTyrPheProGluProValThrValSerTrp
TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGG
ACCCGACGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACC

551 AsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGln
 AACTCAGGCGCTCTGACCAGCGGCGTGACACCTTCCCAGCTGTCCTACA
 TTGAGTCCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGT

601 •SerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerAsn
 GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCA
 CAGGAGTCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCTGT

651 ••PheGlyThrGlnThrTyrThrCysAsnValAspHisLysProSerAsn
 ACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAAC
 TGAAGCCGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTTCGGGTCGTTG

701 ThrLysValAspLysThrVal
 ACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGT
 TGGTTCACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCA

751 GTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGT
 CAGACGACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACA

801 GCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTACCCG
 CGTCGGGGTCGGGTCCCGTCGTTCGGTCCGGGGTAGACAGAGGAGTGGGC

851 GAGGCCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTT
 CTCCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTCCAGAAGACCGAAA

901 TTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCAGGGCC
 AAGTGGTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGG

951 TTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCC
 AAGTGTGTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTTCGGTATAGG

1001 GGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCA
 CCTCCTGGGACGGGGACTGGATTCCGGCTGGGGTTTTCCGGTTTGACAGGT

1051 CTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAA
 GAGGGAGTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTT

1101 GluArgLysCysCysValGluCysProProCysPro
 TCTTCTCTCTGCAGAGCGCAAATGTTGTGTGTCGAGTGCCACCGTGCCAG
 AGAAGAGAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCT

1151 GTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCT
 CATTCGGTCCGGTCCGGAGCGGGAGGTGAGTTCCGCCCTGTCCACGGGA

1201 AGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCA
 TCTCATCGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGT

1251 AlaProProValAlaGlyProSerValPheLeu
 CCTCCATCTCTTCCTCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTC
 GGAGGTAGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAG

1301 PheProProLysProLysAspThrLeuMetIleSerArgThrProGluVal
 TTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
 AAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA

1351 •ThrCysValValValAspValSerHisGluAspProGluValGlnPheAsn
 CACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA
 GTGCACGCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGT

1401 ••TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArg
 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGG
 TGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCC

1451 GluGluGlnPheAsnSerThrPheArgValValSerValLeuThrValVal
 GAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGT
 CTCCTCGTCAAGTTGTCTGTGCAAGGCACACCAGTCGCAGGAGTGGCAACA

1501 •HisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys
 GCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
 CGTGGTCCTGACCGACTTGCCGTTCTCATGTTACGTTCCAGAGGTTGT

1551 ••GlyLeuProAlaProIleGluLysThrIleSerLysThrLys
 AAGGCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGG
 TTCCGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTGGTTTCCACCC

1601 ACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCACCCCT
 TGGGCGCCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGA

1651 GlyGlnPro
 CTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC
 GACGGGACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGG

1701 ArgGluProGlnValTyrThrLeuProProSerArgGluGluMetThrLys
 CGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAA
 GCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGTT

1751 •AsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle
 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACA
 CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTTCGTGT

1801 ••AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr
 TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC
 AGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG

1851 ThrProProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeu
ACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCT
TGTGGAGGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCTGA

1901 ·ThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerVal
CACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
GTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAAGAGTACGAGGC

1951 ··MetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGAC

2001 SerProGlyLys
TCTCCGGGTAAA
AGAGGCCCATTT

FIGURE 45

1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeu
ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGC
TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACG

51 ••LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
TGCTCTGGTTCCCAGGCGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
ACGAGACCAAGGGTCCGCGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

101 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCCG

151 •SerGlnAspIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
AAGTCAGGACATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
TTCAGTCCTGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

201 ••AlaProLysArgLeuIleTyrAlaAlaSerAsnLeuGlnSerGlyVal
AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAATTTGCAAAGTGGGGTC
TTCGGGGATTTCGCGGACTAGATACGACGTAGGTTAAACGTTTCACCCAG

251 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
CCATCAAGGTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAT
GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

301 •SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
GTCGTCGGACGTGCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

351 ••SerTyrProProThrPheGlyGlyGlyThrLysValGluIleLysArg
ATAGCTACCCTCCCCTTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGA
TATCGATGGGAGGGTGAAAGCCGCCTCCCTGGTTCCACCTTTAGTTTGCT

401 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

451 •LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
GAAATCTGGAACTGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

501 ••GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
GAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAAC
CTCTCCGGTTTTCATGTACACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
551 TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCTGTCGTGGATGTCGGA

•SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
601 CAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

••AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
651 ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

PheAsnArgGlyGluCys
701 TTCAACAGGGGAGAGTGT
AAGTTGTCCCCTCTCACA

FIGURE 46

1 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
ATGAAACACCTGTGGTTCTTCCTTCTCCTGGTGG
TACTTTGTGGACACCAAGAAGGAAGAGGACCACC

51 ··AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
CAGCTCCCAGATGGGTCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCA
GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCCGGT

101 GlyLeuValLysProSerGluThrLeuSerLeuThrCysThrValSerGly
GGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGG
CCTGACCACTTCGGAAGCCTCTGGGACAGGGAGTGGACGTGACAGAGACC

151 ·ValSerIleSerAsnTyrTyrTrpSerTrpIleArgGlnSerProGlyLys
TGTCTCCATCAGTAATTACTACTGGAGCTGGATCCGGCAGTCCCCAGGGA
ACAGAGGTAGTCATTAATGATGACCTCGACCTAGGCCGTCAGGGGTCCCT

201 ··GlyLeuGluTrpIleGlyTyrIleTyrTyrSerGlySerProTyrTyr
AGGGACTGGAGTGGATTGGATATATCTATTACAGTGGGAGTCCCTATTAC
TCCCTGACCTCACCTAACCTATATAGATAATGTCACCCTCAGGGATAATG

251 AsnProSerLeuLysSerArgValThrIleSerAlaAspThrSerLysAsn
AACCCTCCCTCAAGAGTCGAGTCACTATATCTGCAGACACGTCCAAGAA
TTGGGGAGGGAGTTCTCAGCTCAGTGATATAGACGTCTGTGCAGGTTCTT

301 ·GlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaIleTyr
CCAATTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCATTT
GGTTAAGAGGGACTTCGACTCGAGACACTGGCGACGCTGTGCCGGTAA

351 ··TyrCysAlaArgGluLysLeuGlyIleGlyAspTyrTrpGlyGlnGly
ATTACTGTGCGAGAGAAAACTGGGGATTGGAGACTACTGGGGCCAGGGA
TAATGACACGCTCTCTTTTGACCCCTAACCTCTGATGACCCCGGTCCCT

401 ThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro
ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
TGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCAGAAGGG

451 ·LeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCys
CCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCT
GGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTGCGCGGGACCCGA

501 ··LeuValLysAspTyrPheProGluProValThrValSerTrpAsnSer
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCA
CGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGT

551 GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer
 GGCCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTC
 CCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAG

601 ·GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGly
 AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCG
 TCCTGAGATGAGGGAGTCGTGCGACCACTGGCACGGGAGGTCGTTGAAGC

651 ··ThrGlnThrTyrThrCysAsnValAspHisLysProSerAsnThrLys
 GCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAG
 CGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCCGGTTCGTTGTGGTTC

701 ValAspLysThrVal
 GTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGC
 CACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCACAGACG

751 TGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCC
 ACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGG

801 CCAGCCCAGGGCAGCAAGGCAGGCCCATCTGTCTCCTCACCCGGAGGCC
 GGTCCGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGG

851 TCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCAC
 AGACGGGCGGGTGAGTACGAGTCCCTCTCCCAGAAGACCGAAAAAGGTG

901 CAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCAGGCCCTTCACA
 GTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGGAAGTGT

951 CACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGG
 GTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTCCGGTATAGGCCCTCC

1001 ACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCT
 TGGGACGGGGACTGGATTCGGCTGGGGTTTCCGGTTTGACAGGTGAGGGA

1051 CAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCT
 GTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTTAGAAGA

1101 GluArgLysCysCysValGluCysProProCysPro
 CTCTGCAGAGCGCAAATGTTGTGTGTCGAGTGCCACCGTGCCAGGTAAGC
 GAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCG

1151 CAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTA
 GTCGGGTCCGGAGCGGGAGGTCGAGTTCCGCCCTGTCCACGGGATCTCAT

1201 GCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCA
 CGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGTGGAGGT

AlaProProValAlaGlyProSerValPheLeuPhePro
 1251 TCTCTTCCTCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTTCCCC
 AGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGG

ProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCys
 1301 CCAAAACCCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTACAGTG
 GGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGCAC

•ValValValAspValSerHisGluAspProGluValGlnPheAsnTrpTyr
 1351 CGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT
 GCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCA

••ValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu
 1401 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAG
 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTC

GlnPheAsnSerThrPheArgValValSerValLeuThrValValHisGln
 1451 CAGTTCAACAGCACGTTCGGTGTGGTCAGCGTCCTCACC GTTGTGCACCA
 GTCAAGTTGTCTGTGCAAGGCACACCAGTCGCAGGAGTGGCAACACGTGGT

•AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeu
 1501 GGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCC
 CCTGACCGACTTGCCGTTCTCATGTTACGTTCCAGAGGTTGTTTCCGG

••ProAlaProIleGluLysThrIleSerLysThrLys
 1551 TCCCAGCCCCATCGAGAAAACCATCTCCAAACCAAAGGTGGGACCCGC
 AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTTGGTTTCCACCCTGGGCG

1601 GGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTCTGCCC
 CCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGG

GlyGlnProArgGlu
 1651 TGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA
 ACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTT

ProGlnValTyrThrLeuProProSerArgGluGluMetThrLysAsnGln
 1701 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
 GGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGT

•ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal
 1751 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCG
 CCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGC

••GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro
 1801 TGGAGTGGGAGAGCAATGGGCAGCCGGAGACAACACTACAAGACCACACCT
 ACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGTGGA

ProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrVal
1851 CCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGT
GGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA

•AspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMethHis
1901 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACG

••GluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerPro
1951 ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
TACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGC

GlyLys
2001 GGTA
CCATTT

FIGURE 47

1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeu
 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGC
 TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACG

51 ••LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
 TGCTCTGGTTCACAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
 ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

101 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
 TCCTCCCTGTCTGCATCTGTCTGGAGACAGAGTCACCATCACTTGCCGGGC
 AGGAGGGACAGACGTAGACAGCCTCTGTCTCAGTGGTAGTGAACGGCCCCG

151 •SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
 AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
 TTCAGTCCCGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

201 ••AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
 AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
 TTCGGGGATTTCGGGACTAGATACGACGTAGGTCAAACGTTTCACCCAG

251 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
 CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCACCTCTCACAAT
 GGTAGTTCCAAGTCGCCGTACCTAGACCCTGTCTTAAGTGAGAGTGTTA

301 •SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
 CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
 GTCGTCTGGACGTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

351 ••SerTyrProProThrPheGlyProGlyThrLysValAspIleLysArg
 ATAGTTACCCTCCCACCTTTTCGGCCCTGGGACCAAGGTGGATATCAAACGA
 TATCAATGGGAGGGTGAAAGCCGGGACCCTGGTTCCACCTATAGTTTGCT

401 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
 ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
 TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

451 •LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
 GAAATCTGGAAGTCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
 CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

501 ••GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
 GAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAAC
 CTCTCCGGTTTCATGTACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

551 SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCCTGTCGTGGATGTCGGA

601 ·SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
CAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
GTCGTGCTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

651 ··AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

701 PheAsnArgGlyGluCys
TTCAACAGGGGAGAGTGT
AAGTTGTCCCCTCTCACA

FIGURE 48

1 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
ATGAAACATCTGTGGTTCTTCCTTCTCCTGGTGG
TACTTTGTAGACACCAAGAAGGAAGAGGACCACC

51 ··AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
CAGCTCCCAGATGGGTCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCA
GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCGGT

101 GlyLeuValLysProSerGluThrLeuSerLeuThrCysThrValSerGly
GGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGG
CCTGACCACTTCGGAAGCCTCTGGGACAGGGAGTGGACGTGACAGAGACC

151 ·GlySerIleSerArgTyrTyrTrpSerTrpIleArgGlnProProGlyLys
TGGCTCCATCAGTCGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGA
ACCGAGGTAGTCAGCAATGATGACCTCGACCTAGGCCGTCGGGGGTCCCT

201 ··GlyLeuGluTrpIleGlyTyrValSerTyrSerGlySerThrTyrTyr
AGGGACTGGAGTGGATTGGGTATGTCTCTTACAGTGGGAGCACCTACTAC
TCCCTGACCTCACCTAACCATAACAGAGAATGTCACCCCTCGTGGATGATG

251 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsn
AACCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAA
TTGGGGAGGGAGTTCTCAGCTCAGTGGTATAGTCATCTGTGCAGGTCTT

301 ·GlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyr
CCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGT
GGTCAAGAGGGACTTCGACTCGAGACACTGGCGACGCTGTGCCGGCACA

351 ··TyrCysAlaArgAspLysLeuGlyIleGlyAspTyrTrpGlyGlnGly
ATTACTGTGCGAGAGATAAACTGGGGATTGGAGACTACTGGGGCCAGGGA
TAATGACACGCTCTCTATTTGACCCCTAACCTCTGATGACCCCGGTCCCT

401 ThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro
ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
TGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCAGAAGGG

451 ·LeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCys
CCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCT
GGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTGCGCGGGACCCGA

501 ··LeuValLysAspTyrPheProGluProValThrValSerTrpAsnSer
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCA
CGGACCAGTTCTGATGAAGGGCTTGGCCACTGCCACAGCACCTTGAGT

551 GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer
 GCGCTCTGACCAGCGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTC
 CCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAG

601 •GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGly
 AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCG
 TCCTGAGATGAGGGAGTCGTGCGACCACTGGCACGGGAGGTCGTTGAAGC

651 ••ThrGlnThrTyrThrCysAsnValAspHisLysProSerAsnThrLys
 GCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAG
 CGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTGTGGTTC

701 ValAspLysThrVal
 GTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGC
 CACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCACAGACG

751 TGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCC
 ACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGG

801 CCAGCCCAGGGCAGCAAGGCAGGCCCATCTGTCTCCTCACCCGGAGGCC
 GGTCGGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGG

851 TCTGCCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCAC
 AGACGGGCGGGGTGAGTACGAGTCCCTCTCCAGAAGACCGAAAAAGGTG

901 CAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACA
 GTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGGAAGTGT

951 CACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGG
 GTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTTCGGTATAGGCCCTCC

1001 ACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCT
 TGGGACGGGGACTGGATTGCGGTGGGGTTTCCGGTTTGACAGGTGAGGGA

1051 CAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCT
 GTCGAGCCTGTGGAAGAGAGAGGGTCTAGGCTCATTGAGGGTTAGAAGA

1101 GluArgLysCysCysValGluCysProProCysPro
 CTCTGCAGAGCGCAAATGTTGTGTGTCGAGTGCCCACCGTGCCCAGGTAAGC
 GAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCC

1151 CAGCCCAGGCCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTA
 GTCGGGTCCGGAGCGGGAGGTTCGAGTTCCGCCCTGTCCACGGGATCTCAT

1201 GCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCA
 CGGACGTAGGTCCCTGTCCGGGGTGCACCCACGACTGTGCAGGTGGAGGT

AlaProProValAlaGlyProSerValPheLeuPhePro
1251 TCTCTTCCTCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTCCCC
AGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGG

ProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCys
1301 CCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTG
GGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGCAC

•ValValValAspValSerHisGluAspProGluValGlnPheAsnTrpTyr
1351 CGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT
GCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCA

••ValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu
1401 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAG
TGCACCTGCCGCACCTCCACGTATTACGGTCTGTTCGGTGCCCTCCTC

GlnPheAsnSerThrPheArgValValSerValLeuThrValValHisGln
1451 CAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACC GTTGTGCACCA
GTCAAGTTGTCTGTGCAAGGCACACCAGTCGCAGGAGTGCCAACACGTGGT

•AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeu
1501 GGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCC
CCTGACCGACTTGCCGTTCTCATGTTACGTTCCAGAGGTTGTTTCCGG

••ProAlaProIleGluLysThrIleSerLysThrLys
1551 TCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGTGGGACCCGC
AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTGGTTTCCACCCTGGGCG

GGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCCACCCTCTGCCC
1601 CCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGG

GlyGlnProArgGlu
1651 TGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA
ACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTT

ProGlnValTyrThrLeuProProSerArgGluGluMetThrLysAsnGln
1701 CCACAGGTGTACACCCTGCCCCCATCCCGGAGGAGATGACCAAGAACCA
GGTGTCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGT

•ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal
1751 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCG
CCAGTCGGACTGGACGGACCAAGTTTCCGAAGATGGGGTCGCTGTAGCGGC

••GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro
1801 TGGAGTGGGAGAGCAATGGGCAGCCGAGAACTACAAGACCACACCT
ACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGTGGA

ProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrVal
1851 CCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGT
GGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCA

•AspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHis
1901 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACG

••GluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerPro
1951 ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
TACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGC

GlyLys
2001 GGTAAA
CCATTT

FIGURE 49

1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuLeu
 ATGAGGCTCCCTGCTCAGCTCCTGGGGCTCCTGC
 TACTCCGAGGGACGAGTTCGAGGACCCCGAGGACG

51 ••LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
 TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
 ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCTAGAGGT

101 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
 TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
 AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCCG

151 •SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
 AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCGGGGA
 TTCAGTCCCGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGCCCCCT

201 ••AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
 AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
 TTCGGGGATTTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCCG

251 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
 CCATCAAGGTTCAAGCGGAGTGGATCTGGGACAGAATTCACTCTCACAAT
 GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

301 •SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
 CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
 GTCGTCCGACGTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

351 ••SerTyrProCysSerPheGlyGlnGlyThrLysLeuGluIleLysArg
 ATAGTTACCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGA
 TATCAATGGGCACGTCAAACCGGTCCCCTGGTTCGACCTCTAGTTTGCT

401 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
 ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
 TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

451 •LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
 GAAATCTGGAAGTCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
 CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

501 ••GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
 GAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAAC
 CTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

551 SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCCTGTCGTGGATGTCGGA

601 ·SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
CAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

651 ··AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

701 PheAsnArgGlyGluCys
TTCAACAGGGGAGAGTGT
AAGTTGTCCCCTCTCACA

FIGURE 50

1 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
ATGAAGCATCTGTGGTTCTTCCTCCTGCTGGTGG
TACTTCGTAGACACCAAGAAGGAGGACGACCACC

51 ••AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
CAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCA
GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCTCAGCCCGGGT

101 GlyLeuValLysProLeuGlnThrLeuSerLeuThrCysThrValSerGly
GGACTGGTGAAGCCTTTACAGACCCTGTCCCTCACCTGCACTGTCTCTGG
CCTGACCACTTCGGAAATGTCTGGGACAGGGAGTGGACGTGACAGAGACC

151 •GlySerIleSerSerGlyValTyrTyrTrpSerTrpIleArgGlnHisPro
TGGCTCCATCAGCAGTGGTGTCTTACTACTGGAGCTGGATCCGCCAGCACC
ACCGAGGTAGTCGTCACCACAAATGATGACCTCGACCTAGGCGGTCGTGG

201 ••GlyLysGlyLeuGluTrpIleGlyTyrIleTyrAsnSerLysThrSer
CAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATAACAGTAAGACCTCC
GTCCCTTCCCGGACCTCACCTAACCCATGTAGATATTGTCATTCTGGAGG

251 TyrTyrAsnProSerLeuLysSerArgLeuThrLeuSerValAspThrSer
TATTATAATCCGTCCCTCAAGAGTCGACTTACCCTATCAGTAGACACGTC
ATAATATTAGGCAGGGAGTTCTCAGCTGAATGGGATAGTCATCTGTGCAG

301 •LysAsnGlnPheSerLeuAsnLeuIleSerValThrAlaAlaAspThrAla
TAAGAACCAGTTCTCCCTGAACCTGATCTCTGTGACTGCCGCGGACACGG
ATTCTTGGTCAAGAGGGACTTGGACTAGAGACACTGACGGCGCCTGTGCC

351 ••ValTyrTyrCysAlaArgAspLysLeuGlyIleAlaAspTyrTrpGly
CCGTGTATTACTGTGCGAGAGATAAATTGGGGATCGCGGACTACTGGGGC
GGCACATAATGACACGCTCTCTATTTAACCCCTAGCGCCTGATGACCCCG

401 GlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyProSerVal
CAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT
GTCCCTTGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCGCGGGTAGCCA

451 •PheProLeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeu
CTTCCCCCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCC
GAAGGGGGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTGCGCGGG

501 ••GlyCysLeuValLysAspTyrPheProGluProValThrValSerTrp
TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGG
ACCCGACGGACCAAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACC

551 AsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGln
 AACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACA
 TTGAGTCCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGT

601 •SerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerAsn
 GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCA
 CAGGAGTCCTGAGATGAGGGAGTCGTGCGACCACTGGCACGGGAGGTCTGT

651 ••PheGlyThrGlnThrTyrThrCysAsnValAspHisLysProSerAsn
 ACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAAC
 TGAAGCCGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCTGGGTCTGTTG

701 ThrLysValAspLysThrVal
 ACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGT
 TGGTTCCACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCA

751 GTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGT
 CAGACGACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACA

801 GCAGCCCCAGCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCG
 CGTCGGGGTTCGGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGC

851 GAGGCCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTT
 CTCCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTCCCAGAAGACCGAAA

901 TTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCAGGCCC
 AAGGTGGTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGG

951 TTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCC
 AAGTGTGTGTCCCGTCCACGAACCGAGTCTGGACGGTTTTTCGGTATAGG

1001 GGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCA
 CCCTCCTGGGACGGGGACTGGATTCCGGCTGGGGTTTTCCGGTTTTGACAGGT

1051 CTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAA
 GAGGGAGTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTT

1101 GluArgLysCysCysValGluCysProProCysPro
 TCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCACCGTGCCAG
 AGAAGAGAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCT

1151 GTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCT
 CATTCCGTTCGGGTCCGGAGCGGGAGGTGAGTTCCGCCCTGTCCACGGGA

1201 AGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCA
 TCTCATCGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGT

AlaProProValAlaGlyProSerValPheLeu
1251 CCTCCATCTCTTCCTCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTC
GGAGGTAGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAG

PheProProLysProLysAspThrLeuMetIleSerArgThrProGluVal
1301 TTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
AAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA

•ThrCysValValValAspValSerHisGluAspProGluValGlnPheAsn
1351 CACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA
GTGCACGCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGT

••TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArg
1401 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGG
TGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCC

GluGluGlnPheAsnSerThrPheArgValValSerValLeuThrValVal
1451 GAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACC GTTGT
CTCCTCGTCAAGTTGTCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACA

•HisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys
1501 GCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
CGTGGTCCTGACCGACTTGCCGTTCTCATGTTACGTTCCAGAGGTTGT

••GlyLeuProAlaProIleGluLysThrIleSerLysThrLys
1551 AAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGG
TTCCGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTGGTTTCCACCC

ACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCACCCCT
1601 TGGGCGCCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGA

GlyGlnPro
1651 CTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC
GACGGGACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGG

ArgGluProGlnValTyrThrLeuProProSerArgGluGluMetThrLys
1701 CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAA
GCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTT

•AsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle
1751 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACA
CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGT

••AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr
1801 TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACC
AGCGGCACCTCACCTCTCGTTACCCGTGCGCCTCTTGTTGATGTTCTG

ThrProProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeu
1851 ACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCT
TGTGGAGGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGA

•ThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerVal
1901 CACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
GTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC

••MetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu
1951 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGAC

SerProGlyLys
2001 TCTCCGGGTAAA
AGAGGCCCATTT

FIGURE 51

1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeu
ATGAGGGTCCCTGCTCAGCTCCTGGGGCTCCTGC
TACTCCCAGGGACGAGTCGAGGACCCCGAGGACG

51 ••LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

101 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgThr
TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGAC
AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCTG

151 •SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
TTCAGTCCCATAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

201 ••AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
TTCGGGGATTTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCAG

251 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCATCTCACAAAT
GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

301 •SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
CAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATA
GTCGTCCGGACGTCCGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

351 ••SerTyrProProThrPheGlyGlyGlyThrLysValGluIleLysArg
ATAGCTACCCTCCCACCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA
TATCGATGGGAGGGTGAAAGCCGCCTCCCTGGTTCCACCTCTAGTTTGCT

401 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

451 •LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
GAAATCTGGAAGTCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

501 ••GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
GAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAAC
CTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

551 SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCCTGTCGTGGATGTCGGA

601 ·SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
CAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

651 ··AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTCCTCG

701 PheAsnArgGlyGluCys
TTCAACAGGGGAGAGTGT
AAGTTGTCCCCTCTCACA